

the Gram-positive anaerobic eubacterium *Clostridium pasteurianum* strain W5, which indicates that the growth factor is not ubiquitous in bacteria.

Using a growth medium supplemented with filter-sterilized extract from mixed H₂-PCE cultures and ABSS (14), we isolated the PCE-dechlorinating organism (strain 195) by a 10⁻⁷ dilution to liquid H₂-PCE medium containing ampicillin (0.3 g/liter). These cultures, when transferred several times in the absence of ampicillin, showed no morphotypes other than irregular cocci. No visible growth was detected by tests for contamination (with a sensitivity of about

10 organisms per milliliter) with basal growth medium amended with lactate, sulfate, or thiosulfate to detect sulfate reducers, yeast extract (0.2 g/liter) to detect fermentative heterotrophs, or Brewer's thioglycollate medium (Difco) to detect fermentative heterotrophs.

Growth of strain 195 on H₂ and PCE was measured by direct microscopic cell counts and cell protein during metabolism of PCE to vinyl chloride (VC) and ETH (Fig. 2, A and B). Cultures continued to grow until day 5, with a doubling time of about 19.2 hours. After day 5, growth ceased but PCE dechlorination continued, which suggests

uncoupling of growth and dechlorination. Cultures receiving H₂ but not PCE showed only slight growth, and PCE dechlorination products were not detected in uninoculated cultures. The amount of VC and ETH produced represented more than 90% of the PCE added to inoculated cultures. The protein yield for days 1 through 5 was 4.8 ± 0.3 g of protein per mole of chloride released; a specific activity of 69.0 ± 10.5 nmol of chloride released per minute per milligram of protein was determined.

Analysis of the conversion of PCE to ETH by a culture of strain 195 that had received five previous doses of PCE showed that PCE was metabolized to VC at a rate of 40 μmol per hour per liter of culture medium, with little buildup of intermediates (Fig. 2C). VC dechlorination to ETH commenced after PCE depletion and could be fit by first-order kinetics with a half-life of about 80 hours for the first 300 hours and of about 150 hours thereafter. This indicated a decay with time in the ability of the culture to metabolize VC. These results resemble those for the mixed methanol-PCE culture from which it was derived (13), except that the mixed culture dechlorinated VC more rapidly relative to PCE. If strain 195 is responsible for VC dechlorination in those mixed cultures, then some factor, perhaps nutritional, limits the rate of VC dechlorination in the pure culture. It is also possible that there is another organism or strain present in the mixed culture that is capable of more rapid VC metabolism.

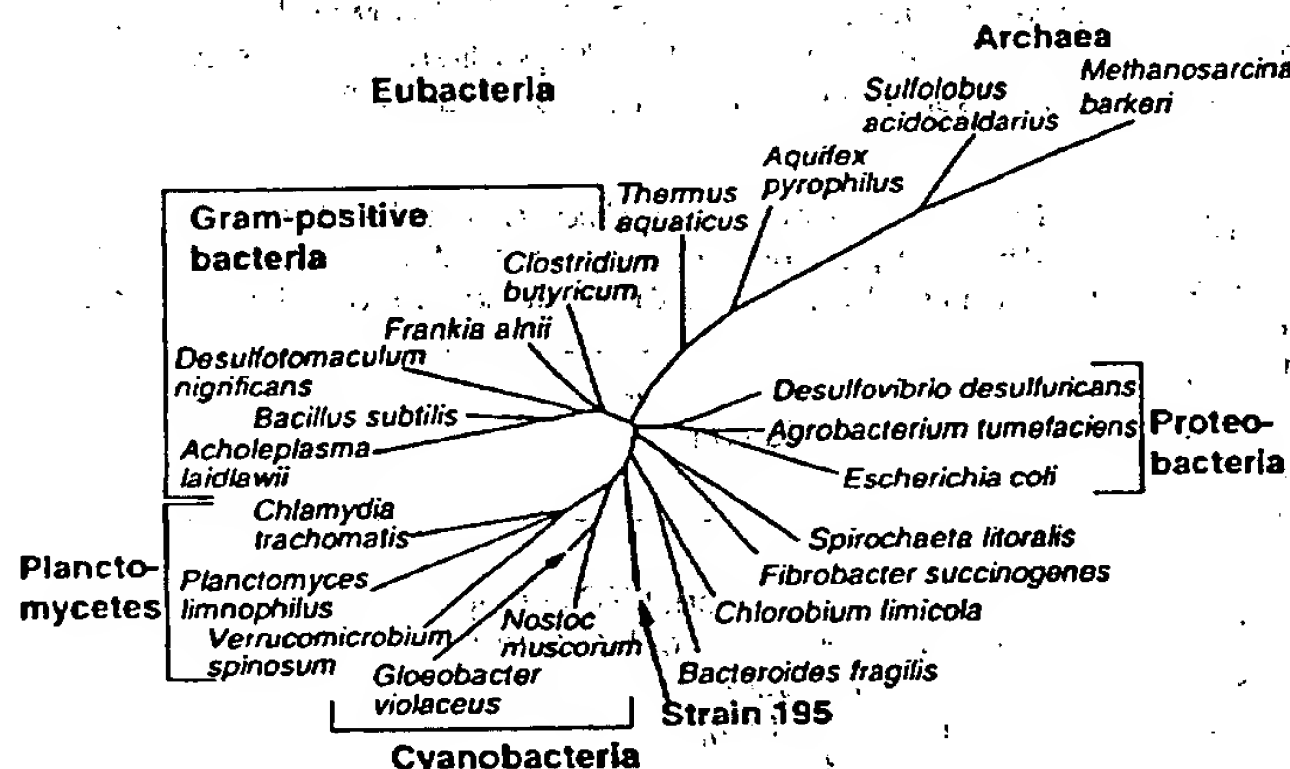
Physiological characterization of strain 195 revealed that it required H₂ for PCE reduction and that it grew only when both H₂ and PCE were present (Fig. 2). Potential electron donors that supported neither PCE dechlorination, nor growth in the absence of PCE, were methanol, pyruvate, lactate, ethanol, formate, glucose, and yeast extract. Potential electron acceptors that did not support growth or were not reduced when H₂ was provided as the electron donor included sulfate, sulfite, thiosulfate, nitrate, nitrite, fumarate, and oxygen (2 or 21%). The culture could reductively dechlorinate 1,2-dichloroethane and 1,2-dibromoethane to ETH, as did the original enrichment culture (13).

Electron microscopic examination (16) of strain 195 (Fig. 3, A and B) revealed small, irregular coccoid cells with an unusual cell wall ultrastructure that resembled the S-layer protein subunit type of cell walls found in many Archaea (17). To test for the presence of a peptidoglycan cell wall, we used fluorescently labeled wheat germ agglutinin, which specifically binds to N-acetylglucosamine and N-acetylneuraminic acid (18). This stain bound to whole cells of the Gram-positive eubacterium *C. pasteurianum*



Fig. 3. Thin-section electron micrographs of coccoid (A) and flattened (B) cells of strain 195 stained with uranyl acetate. Scale bar, 0.2 μm. Phase-contrast (C) and epifluorescence (D) micrographs of cell wall preparations of *E. coli* DH5α stained with fluorescein-labeled wheat germ agglutinin (100 mg/liter) (Molecular Probes) (18). Phase-contrast (E) and epifluorescence (F) micrographs of cell wall preparations of strain 195 stained with wheat germ agglutinin. Cell wall samples for (C) through (F) were prepared by lysing the cells in boiling 4% SDS in 25 mM phosphate buffer (pH 7) (20) followed by heat fixation to a microscope slide and washing with distilled water to remove SDS and other chemicals before staining. Scale bar in (C) [for (C) through (F)], 5 μm.

Fig. 4. Unrooted phylogenetic tree generated for the 16S ribosomal DNA sequence (GenBank database number AF004928) from strain 195 with the use of the SUGGEST TREE maximum-likelihood program provided by the Ribosome Database Project (RDP) (21). DNA was extracted from strain 195 as described (22). The sequence was amplified as a polymerase chain reaction product with the use of primers 27f and



1522r under standard conditions (23), followed by cloning with the Invitrogen (San Diego, California) TA cloning kit and sequencing with an Applied Biosystems model 373 analyzer operated by the Cornell Biotechnology Institute. Eight sequencing primers were used (23), including two against the vector, resulting in only a single ambiguous base in the entire sequence. For simplicity, some organisms included in the original analyses have been deleted from the figure. Other analyses of these sequences were performed by manually aligning the sequence of strain 195 to other prealigned sequences from the RDP, followed by the use of the PHYLIP 3.5c package (24), including DNAML (maximum-likelihood analysis), and DNADIST (Kimura model) coupled to either FITCH or NEIGHBOR.

WF (15) and to cell wall preparations of the Gram-negative eubacterium *E. coli* DH5 α (Fig. 3, C and D) (18). No binding was detected for whole cells (15) or for cell wall preparations (Fig. 3, E and F) of strain 195.

The phylogenetic position of strain 195 was determined on the basis of its 16S ribosomal DNA sequence (Fig. 4). The PCE dechlorinator grouped within the eubacteria in all analyses but did not cluster within any of the known phylogenetic lines. Although the maximum likelihood analysis presented places strain 195 on a branch that includes cyanobacteria and planctomycetes, DNA distance analyses placed it closer to *Clostridium butyricum* and its relatives (19) but with little affiliation for other members of the Gram-positive branch. Thus, its relationship with the presently described eubacterial branches is unclear at this time. It is clearly distinct from other recent isolates that reduce PCE to *cis*-DCE (9), which are affiliated with the ϵ and γ branches of the Proteobacteria or with the Gram-positive sulfate-reducing bacteria. Because strain 195 does not appear to belong to any presently known genus or species, we suggest naming it *Dehalococcoides ethenogenes* strain 195, pending a more thorough taxonomic description.

In summary, we isolated an organism that is capable of respiratory reductive dechlorination of PCE completely to ETH with H₂ as an electron donor. Previous isolates reduce PCE only as far as *cis*-DCE. It is of interest that at many PCE-contaminated sites, dechlorination proceeds only as far as *cis*-DCE, whereas at other sites VC and ETH are produced (3). It is not clear whether incomplete dechlorination at a given site is due to suboptimal physiochemical conditions, deficiencies in electron donors or nutrients present, or a lack of appropriate organisms.

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Membrane and Morphological Changes in Apoptotic Cells Regulated by Caspase-Mediated Activation of PAK2

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Apoptosis of Jurkat T cells induced the caspase-mediated proteolytic cleavage of p21-activated kinase 2 (PAK2). Cleavage occurred between the amino-terminal regulatory domain and the carboxyl-terminal catalytic domain, which generated a constitutively active PAK2 fragment. Stable Jurkat cell lines that expressed a dominant-negative PAK mutant were resistant to the Fas-induced formation of apoptotic bodies, but had an enhanced externalization of phosphatidylserine at the cell surface. Thus, proteolytic activation of PAK2 represents a guanosine triphosphatase-independent mechanism of PAK regulation that allows PAK2 to regulate morphological changes that are seen in apoptotic cells.

Apoptosis, or regulated cell death, is a fundamental process in the development of multicellular organisms. Although it is initiated by many physiologic and pathologic stimuli, all apoptotic cells undergo a similar sequence of morphological and biochemical events (1). The cascade of ICE/CED-3 family cysteine proteases (termed caspases) (2) is a common and critical component of the cell death pathway (3, 4). The identified targets for proteolytic cleavage by caspases are few, and the role of individual targets in mediating particular apoptotic events remains ill-defined.

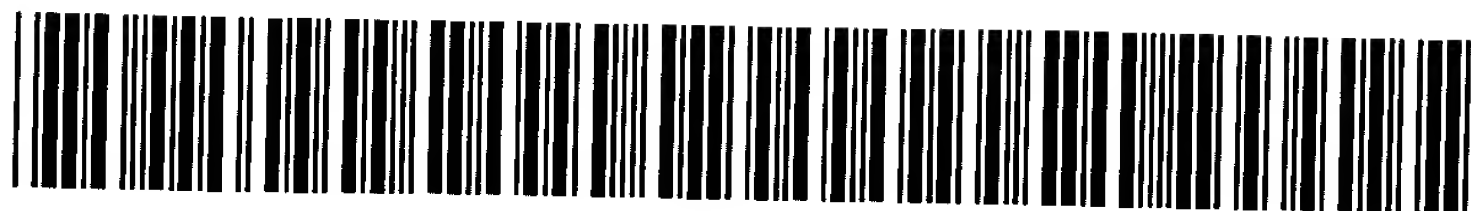
p21-activated kinases (PAKs) are serine-threonine kinases whose activity is regulated by the small guanosine triphosphatases (GTPases) Rac and Cdc42 (5, 6). PAKs regulate morphological and cytoskeletal

changes in a variety of cell types (7, 8), implicating PAKs as downstream mediators of the effects of Rac and Cdc42 on the actin cytoskeleton. Immunoblot analysis (9) reveals that Jurkat T cells predominantly express the 62-kD PAK2 isoform. An apparent decrease in the intensity of the 62-kD PAK2 band is observed after induction of Jurkat cell death by Fas receptor cross-linking (10). A 34-kD COOH-terminal PAK2 fragment (Fig. 1A) and a 28-kD NH₂-terminal PAK2 fragment (Fig. 1B) appeared after 1 hour, suggesting that PAK2 is cleaved into two defined fragments during Fas-induced apoptosis (11). In detailed time-course studies, PAK2 cleavage was detected as early as 30 min after stimulation by immunoglobulin M (IgM) antibody to Fas (anti-Fas) and the cleavage of PAK2 always correlated with the onset of apoptotic cell death. PAK2 cleavage was also observed when apoptosis was induced in Jurkat cells with C2 ceramide or in MCF-7 cells with tumor necrosis factor- α (TNF- α) (Fig. 1C), suggesting that this is a general phenomenon in apoptotic cells.

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IMIS
Internal Misc. Paper

LET.
Misc. Incoming Letter

371P
PCT Papers in a 371 Application

A...
Amendment Including Elections

ABST
Abstract

ADS
Application Data Sheet

AF/D
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APPENDIX
Appendix

ARTIFACT
Artifact

BIB
Bib Data Sheet

CLM
Claim

COMPUTER
Computer Program Listing

CRFL
All CRF Papers for Backfile

DIST
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DRW
Drawings

FOR
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FRPR
Foreign Priority Papers

IDS
IDS Including 1449

NPL
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Oath or Declaration

PET.
Petition

RETMAIL
Mail Returned by USPS

SEQLIST
Sequence Listing

SPEC
Specification

SPEC NO
Specification Not in English

TRNA
Transmittal New Application

CTNF
Count Non-Final

CTRS
Count Restriction

EXIN
Examiner Interview

M903
DO/EO Acceptance

M905
DO/EO Missing Requirement

NFDR
Formal Drawing Required

NOA
Notice of Allowance

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OUTGOING

CTMS
Misc. Office Action

1449
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892
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ABN
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APDEC
Board of Appeals Decision

APEA
Examiner Answer

CTAV
Count Advisory Action

CTEQ
Count Ex parte Quayle

CTFR
Count Final Rejection

INCOMING

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Change of Address

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Applicant Remarks in Amendment

XT/
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Evidence Copy Box Identification

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<p>(54) Title: NUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION OF DECHLORINATING BACTERIA</p> <p>(57) Abstract</p> <p>A unique 16S rRNA profile derived from <i>Dehalococcoides ethenogenes</i> has been identified and isolated. The profile contains a nucleic acid fragment that is linked to dechlorinating activity. This sequence is set forth in SEQ ID NO:1.</p>		

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TITLENUCLEIC ACID FRAGMENTS FOR THE IDENTIFICATION
OF DECHLORINATING BACTERIAFIELD OF THE INVENTION

5 The invention relates to the field of molecular biology and microbiology. More specifically, 16S rRNA regions of been identified and isolated from *Dehalococcoides ethenogenes* that enable the identification of dechlorinating bacterial strains. Probes and primers corresponding to the unique regions have been constructed to enable the rapid identification of the dechlorinators.

BACKGROUND

10 Groundwater pollution by halogenated, and particularly chlorinated solvents is a worldwide problem associated primarily with industrial sites where mishandling or improper disposal has brought these solvents in contact with the soil. The most common and problematic compounds are the chlorinated ethylenes
15 (ethenes) such as tetra- tri- or di-chloroethylene. Carbon tetrachloride, chloroform and methylene chloride are also pervasive pollutants. The reasons for concern are basically threefold. First, most of these solvents are sparingly soluble in water and have the tendency to stick to soil particles. This results in tenacious underground plumes of solvent which cannot readily be removed by standard
20 pump and treat technology (Biswas, N., et al., *Water Environ. Res.* 64, 170, 10, 1 (1992); Hutter, G. M., et. al., *Water Environ. Res.* 64, 69, (1992)). Second, the toxicology of many chlorinated solvents suggests that these compounds may be carcinogenic and damaging to specific organs such as the liver and kidneys (Price, P. S., Memo of the U.S. Environmental Protection Agency, Office of Water,
25 Washington, D.C.(1985); Vogel, T. M., *Environ. Sci. Technol.*, 21, 722, (1987)). Finally, under conditions found in many aquifers and subsurface environments, chlorinated ethylenes and methanes are very slow to be degraded biologically. The result of these factors is that chlorinated solvents are long-lived potentially hazardous groundwater pollutants.

30 Currently there are two approaches to in situ removal of organohalogen pollutants. The first approach is the standard "pump and treat" method where groundwater is pumped to the surface for physical stripping of the contaminant from the water. For chlorinated solvents this is more of a containment method than a remediation technology although given sufficient time (typically decades to
35 centuries) this method may capture most of the pollutant. The other approach is biological in nature and utilizes microorganisms for the enzymatic transformation of the halogenated organics. The biological approach may utilize microorganisms indigenous to a particular site where the remediation process consists primarily of

making additions to the contaminated site that enhance the growth of the desired microorganism. Alternatively, nonindigenous microorganisms may be introduced to a contaminated site with the necessary amendments needed for growth.

A number of organisms are known to dechlorinate persistent chlorinated pollutants. For example, *Dehalobacter restrictus* and *Dehalospirillum multivorans*, have been shown to partially dechlorinate chlorinated ethenes (Kochian et al., *Plant Mol. Biol.* 46:237 (1995); Delhaize et al., *Plant Physiol.* 107:315 (1995)). Similarly, *Dehalococcoides ethenogenes* has been shown to effect the complete dechlorination of tetrachloroethene and trichloroethene to ethene [Freedman et al., *Appl. Environ. Microbiol.* 55:2144 (1989)] and Maymó-Gatell et al. (*Science*, 176:1568 (1997)) have isolated a *D. ethenogenes* strain that is capable of respiratory reductive dechlorination of tetrachloroethene directly to ethene with hydrogen as an electron donor. Analysis of the 16S rRNA of the Maymó-Gatell organism revealed a unique profile that may be used to identify organisms of similar reductive capabilities.

The first step in utilizing the dechlorinating properties of the above identified organisms is rapid and accurate identification. One method of identification involves the use of DNA probes (see for example in WO 89/06704, U.S. Patent No. 4,851,330, and U.S. Patent No. 5,574,145). Many such probes derive from the observation (see Woese, *Scientific American* 244 (6) 1981 for review) that parts of the 16S and 23s ribosomal RNA (rRNA) sequences vary in different species. This information was used initially for phylogenetic analyses but it has more recently been used for DNA probe-based methods for the identification of organisms. The utility of such a method is based on the conservation of nucleic acid sequence within the rRNA sequences.

Each of the cells of all life forms, except viruses, contain ribosomes and therefore ribosomal RNA. A ribosome contains three separate single strand RNA molecules, namely, a large molecule, a medium sized molecule, and a small molecule. The two larger rRNA molecules vary in size in different organisms. Ribosomal RNA is a direct gene product and is coded for by the rRNA gene. This DNA sequence is used as a template to synthesize rRNA molecules. A separate gene exists for each of the ribosomal RNA subunits. Multiple rRNA genes exist in most organisms, many higher organisms containing both nuclear and mitochondrial rRNA genes. Numerous ribosomes are present in all cells of all life forms. About 85-90 percent of the total RNA in a typical cell is rRNA. A bacteria such as *E. coli* contains about 10^4 ribosomes per cell. Much of the sequences in rRNA highly conserved across broad evolutionary boundaries,

however, certain regions are highly variable and may be used to make fine distinctions between species, sub-species and strains (U.S. Patent No. 5567587).

The problem to be overcome therefore is to identify a unique 16S rDNA sequence in a bacteria capable of dechlorination of persistent chlorinated compounds for the identification and ultimate enhancement of that bacteria to remediate a contaminated site. Applicants have solved the state problem by providing a set of nucleic acid sequences that are unique to various strains of *Dehalococcoides ethenogenes*.

SUMMARY OF THE INVENTION

The present invention provides an isolated 16S rDNA sequence indicative of a dechlorinating bacterial strain selected from the group consisting of: (a) SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:8 and SEQ ID NO:30; (b) an isolated nucleic acid molecule that hybridizes with (a) under the following hybridization conditions: 0.1X SSC, 0.1% SDS at 65 °C; and (c) an isolated nucleic acid molecule that is completely complementary to (a) or (b).

The invention further provides primers useful for the identification of new dechlorinating bacteria selected from the group consisting of: SEQ ID NOs:9-29; and any sequences that hybridize under conditions of 0.1X SSC, 0.1% SDS at 65 °C to those primers.

The invention additionally provides an isolated bacterial strain comprising any one of the sequences of the instant invention as set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6 and SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21 and SEQ ID NO:30, wherein said strain has the ability to dechlorinate chlorinated compounds.

The invention further provides a method for identifying a dechlorinating bacterial strain comprising: (i) extracting genomic DNA from a cell suspected of being able to dechlorinate chlorinated compounds; (ii) probing the extracted genomic DNA with a probe derived from any one of the sequences instant invention as set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21 and SEQ ID NO:30, under suitable hybridization conditions, wherein the identification of a hybridizable nucleic acid fragment

confirms the presence of a bacteria capable of dechlorinating chlorinated compounds.

Similarly the invention provides a method for identifying a dechlorinating bacterial strain comprising (i) extracting genomic DNA from a cell suspected of being able to dechlorinate chlorinated compounds; and (ii) amplifying the extracted genomic DNA with an oligonucleotide primer corresponding to a portion of any one of the sequences instant invention as set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21 and SEQ ID NO:30, such that amplification products are generated wherein the presence of amplification products confirms the presence of a dechlorinating bacterial strain.

The invention additionally provides a method for the dechlorination of chlorinated compounds comprising contacting a chlorinated compound with an isolated bacterial strain comprising any one of the DNA fragments as set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, and SEQ ID NO:30 under conditions suitable for dechlorination to occur.

BRIEF DESCRIPTION OF THE DRAWINGS AND SEQUENCE LISTING

Figure 1 is an alignment of 16S rDNA sequence profile from *Dehalococcoides ethenogenes* DHE-195 as disclosed in Maymó-Gatell et al., *Science*, 176:1568 (1997), as compared with profiles generated for organisms isolated from a number of wastewater treatment sites.

Figure 2 is a comparison of the instant dechlorinating 16S rDNA profiles with a 16S rDNA profile from *E. coli*.

Figure 3 is a graph illustrating the ability of a soil microcosm or culture developed from certain soils taken from a chloroethene contaminated site to dechlorinate trichloroethylene or perchloroethylene.

Figure 4 is an image of an electrophoresis gel used to detect PCR products in a test of soils contaminated with chloroethenes using two sets of the primers described herein.

The following sequence descriptions and sequences listings attached hereto comply with the rules governing nucleotide and/or amino acid sequence disclosures in patent applications as set forth in 37 C.F.R. §1.821-1.825. The

Sequence Descriptions contain the one letter code for nucleotide sequence characters and the three letter codes for amino acids as defined in conformity with the IUPAC-IYUB standards described in *Nucleic Acids Research* 13:3021-3030 (1985) and in the *Biochemical Journal* 219 (No. 2):345-373 (1984) which are
5 herein incorporated by reference. The symbols and format used for nucleotide and amino acid sequence data comply with the rules set forth in 37 C.F.R. §1.822.

SEQ ID NO:1 is a unique region of the *Dehalococcoides ethenogenes* 16S rDNA profile which is linked to dechlorinating activity.

10 SEQ ID NO:2 is the 16S rDNA profile of *Dehalococcoides ethenogenes* DHE-PL, isolated from soil surrounding in industrial site.

SEQ ID NO:3 is the 16S rDNA profile of *Dehalococcoides ethenogenes* DHE-STF, isolated from soil surrounding in industrial site.

SEQ ID NO:4 is the 16S rDNA profile of *Dehalococcoides ethenogenes* DHE-DAB, isolated from soil surrounding in industrial site.

15 SEQ ID NO:5 is the 16S rDNA profile of *Dehalococcoides ethenogenes* DHE-PIN, isolated from soil surrounding in industrial site.

SEQ ID NO:6 is the 16S rDNA profile of *Dehalococcoides ethenogenes* DHE-DLL, isolated from soil surrounding in industrial site.

20 SEQ ID NO:7 is the 16S rDNA profile of *Dehalococcoides ethenogenes* DHE-195 as reported in Maymó-Gatell et al. (*Science*, 176:1568 (1997)), Genbank AF004928.

SEQ ID NO:8 is the consensus sequence derived from DHE-PL, DHE-STF, DHE-DAB, DHE-PIN, and DHE-DLL at bases E180-E226.

25 SEQ ID NO:9-29 are primers derived from the 16S rDNA profile, useful in the identification of dechlorinating bacteria.

SEQ ID NO:30 is the consensus sequence derived from DHE-PL, DHE-STF, DHE-DAB, DHE-PIN, and DHE-DLL at bases E1001-E1047.

SEQ ID NO:31 is the base sequence in the region of the consensus 16S rDNA profile from where the diagnostic sequence is derived.

30 SEQ ID NO:32 is the base sequence in the region of the DHE-195 16S rDNA profile from where the diagnostic sequence is derived.

SEQ ID NO:33 is the *E. coli* reference 16S rDNA sequence.

DETAILED DESCRIPTION OF THE INVENTION

35 The present invention provides unique 16S rDNA sequence profiles derived from *Dehalococcoides ethenogenes* (DHE). *D. ethenogenes* is known for its ability to degrade persistent chlorinated pollutants. The instant sequence profiles may be used to identify and sub-type bacteria with similar metabolic pathways. One sequence (ATTTTCTAGCGAGACTGCCCCGCG, SEQ ID

NO:1), beginning at base E1146, has been identified in all DHE's isolated from contaminated soils and is strongly linked to the ability of these organisms to degrade chlorinated organics. Similarly, a stretch of nucleic acids ranging between E180 and E226, corresponding to SEQ ID NO:8 may be used to identify dechlorinators as well as for genetic sub-typing of species.

In this disclosure, a number of terms and abbreviations are used. The following definitions are provided.

The term "*Dehalococcoides ethenogenes*" will be abbreviated "DHE".

The term "DHE-195" will refer to the strains of *Dehalococcoides ethenogenes* isolated and characterized by Maymó-Gatell et al. (*Science*, 176:1568 (1997)).

The terms "DHE-PL, DHE-STF, DHE-DAB, DHE-DLL and DHE-PIN" will refer to strains of *Dehalococcoides sp.* containing the instant dechlorinating 16S rDNA profile.

The term "dechlorinating bacteria" refers to any bacterial species or strain that has the ability to remove at least one chlorine atom from a chlorinated organic compound. Dechlorinating bacteria may have the ability to grow on chlorinated organics as a sole carbon source, or may prefer degradation using an alternate energy source.

The term "chlorinated compounds" will mean any straight chain or ring containing organic compound which contains at least one chlorine atom.

Trichloroethylene will be abbreviated "TCE".

Perchloroethylene will be abbreviated "PCE".

The term "16S rDNA" will refer to the DNA encoding ribosomal RNA found within bacterial cells.

The term "16S rDNA profile" will refer to the specific DNA sequence of the rDNA gene in any particular organism. For the purposes of the present invention the 16S rDNA profiles for DHE-195, DHE-PL, DHE-STF, DHE-DAB, DHE-DLL and DHE-PIN are illustrated in Figures 1 and 2.

The term "signature sequence" or signature sequence region" will refer to those short sequences in the 16S gene or rRNA molecule which are unique to a certain group or groups of organisms. These sequences can be used to define domains, group, subdivisions genera or species of an organism.

The term "consensus sequence" as used herein, as it relates to the alignment of a given set of sequences, will be defined as the sequence of the set of bases where a designated base is the one that occurs most often at each position in the 16S sequence.

The term "reference sequence" as used herein, as it relates to the alignment of a given set of sequences, will be defined as the particular 16S sequence to which the bases at each position of an alignment of 16S sequences are compared. The reference sequence used herein was an *E. coli* 16S rDNA sequence. Bases identified in the reference sequence that correlate to corresponding bases in a 16S rDNA profile are assigned an "E number". Thus, the base labeled E-27 on the reference sequence corresponds to base 1 of the 16S rDNA profile of DHE-195 and E-107 corresponds to base 66 of DHE-195. The complete correlation is given in Table 2.

The term "dechlorinating 16S rDNA profile" will refer to a 16S rDNA profile containing the diagnostic sequence as set forth in SEQ ID NO:1.

The term "diagnostic sequence" will refer to the sequence ATTTTCTAGCGAGACTGCCCCGCG (SEQ ID NO:1) which is indicative of dechlorinating activity.

The letters "A", "G", "T", "C" when referred to in the context of nucleic acids will mean the purine bases Adenine (C₅H₅N₅), Guanine (C₅H₅N₅O) and the pyrimidine bases Thymine (C₅H₆N₂O₂) and Cytosine (C₄H₅N₃O) respectively.

In this disclosure, a number of terms and abbreviations are used. The following definitions are provided.

"Gene" refers to a nucleic acid fragment that expresses a specific protein, including regulatory sequences preceding (5' non-coding sequences) and following (3' non-coding sequences) the coding sequence.

The term "nucleic acid fragment" will refer to a polymer of RNA or DNA that is single- or double-stranded, optionally containing synthetic, non-natural or altered nucleotide bases. A nucleic acid fragment in the form of a polymer of DNA may be comprised of one or more segments of cDNA, genomic DNA or synthetic DNA.

The term "oligonucleotide" refers to primers, probes, oligomer fragments to be detected, labeled-replication blocking probes, oligomer controls, and shall be generic to polydeoxyribonucleotides (containing 2-deoxy-D-ribose), to polyribonucleotides (containing D-ribose) and to any polynucleotide which is an N glycoside of a purine or pyrimidine base (nucleotide), or modified purine or pyrimidine base. Also included in the definition of "oligonucleotide" are nucleic acid analogs (e.g., peptide nucleic acids) and those that have been structurally modified (e.g., phosphorothioate linkages). There is no intended distinction between the length of a "nucleic acid", "polynucleotide" or an "oligonucleotide".

The term "primer" refers to an oligonucleotide (synthetic or occurring naturally), which is capable of acting as a point of initiation of nucleic acid

synthesis or replication along a complementary strand when placed under conditions in which synthesis of a complementary strand is catalyzed by a polymerase.

5 The term "probe" refers to an oligonucleotide (synthetic or occurring naturally), that is significantly complementary to a "fragment" and forms a duplexed structure by hybridization with at least one strand of the fragment.

The term "complementary" is used to describe the relationship between nucleotide bases that are hybridizable to one another. For example, with respect to DNA, adenosine is complementary to thymine and cytosine is complementary to guanine.

10 A nucleic acid molecule is "hybridizable" to another nucleic acid molecule, such as a cDNA, genomic DNA, or RNA, when a single stranded form of the nucleic acid molecule can anneal to the other nucleic acid molecule under the appropriate conditions of temperature and solution ionic strength. Hybridization and washing conditions are well known and exemplified in 15 Sambrook, J., Fritsch, E. F. and Maniatis, T. Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor (1989), particularly Chapter 11 and Table 11.1 therein (entirely incorporated herein by reference). The conditions of temperature and ionic strength determine the "stringency" of the hybridization. For preliminary 20 screening for homologous nucleic acids, low stringency hybridization conditions, corresponding to a T_m of 55°, can be used, e.g., 5X SSC, 0.1% SDS, 0.25% milk, and no formamide; or 30% formamide, 5X SSC, 0.5% SDS. Moderate stringency hybridization conditions correspond to a higher T_m , e.g., 40% formamide, with 25 5X or 6X SSC.

Hybridization requires that the two nucleic acids contain complementary sequences, although depending on the stringency of the hybridization, mismatches between bases are possible. The appropriate stringency for hybridizing nucleic acids depends on the length of the nucleic acids and the degree of 30 complementation, variables well known in the art. The greater the degree of similarity or homology between two nucleotide sequences, the greater the value of T_m for hybrids of nucleic acids having those sequences. The relative stability (corresponding to higher T_m) of nucleic acid hybridizations decreases in the following order: RNA:RNA, DNA:RNA, DNA:DNA. For hybrids of greater 35 than 100 nucleotides in length, equations for calculating T_m have been derived (see Sambrook et al., *supra*, 9.50-9.51, hereby incorporated by reference). For hybridizations with shorter nucleic acids, i.e., oligonucleotides, the position of mismatches becomes more important, and the length of the oligonucleotide

determines its specificity (see Sambrook et al., *supra*, 11.7-11.8, hereby incorporated by reference). In one embodiment the length for a hybridizable nucleic acid is at least about 10 nucleotides. Preferable a minimum length for a hybridizable nucleic acid is at least about 15 contiguous nucleotides; more preferably at least about 20 contiguous nucleotides; and most preferably the length is at least 30 contiguous nucleotides. Thus, where a "probe" or "primer" is "derived from" or corresponds to a "portion" of a nucleic acid fragment, the probe or primer or portion will preferably be at least about 15 contiguous nucleotides; more preferably at least about 20 contiguous nucleotides; and most preferably the length is at least 30 contiguous nucleotides of the fragment from which it is derived. Furthermore, the skilled artisan will recognize that the temperature and wash solution salt concentration may be adjusted as necessary according to factors such as length of the probe.

The term "amplification product" refers to portions of nucleic acid fragments that are produced during a primer directed amplification reaction. Typical methods of primer directed amplification include polymerase chain reaction (PCR), ligase chain reaction (LCR) or Strand displacement Amplification (SDA). If PCR methodology is selected, the replication composition would include for example, nucleotide triphosphates, two primers with appropriate sequences, DNA or RNA polymerase and proteins. These reagents and details describing procedures for their use in amplifying nucleic acids are provided in U.S. Patent No. 4,683,202 (1987, Mullis, et al.) and U.S. Patent No. 4,683,195 (1986, Mullis, et al.). If LCR methodology is selected, then the nucleic acid replication compositions would comprise, for example, a thermostable ligase, e.g., *T. aquaticus* ligase, two sets of adjacent oligonucleotides wherein one member of each set is complementary to each of the target strands, Tris HCl buffer, KCl, EDTA, NAD, dithiothreitol and salmon sperm DNA. See, for example, Tabor et al., *Proc. Acad. Sci. U.S.A.*, 82, 1074-1078 (1985)).

The term "sequence analysis software" refers to any computer algorithm or software program that is useful for the analysis of nucleotide or amino acid sequences. "Sequence analysis software" may be commercially available or independently developed. Typical sequence analysis software will include but is not limited to the GCG suite of programs (Wisconsin Package Version 9.0, Genetics Computer Group (GCG), Madison, Wisc.), BLASTP, BLASTN, BLASTX (Altschul et al., *J. Mol. Biol.* 215:403-410 (1990), and DNASTAR (DNASTAR, Inc., 1228 S. Park St. Madison, WI 53715 USA). Within the context of this application it will be understood that where sequence analysis software is used for analysis, that the results of the analysis will be based on the

"default values" of the program referenced, unless otherwise specified. As used herein "default vales" will mean any set of values or parameters which originally load with the software when first initialized.

Standard recombinant DNA and molecular cloning techniques used here are well known in the art and are described by Sambrook, J., Fritsch, E. F. and Maniatis, T., Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY (1989) (hereinafter "Maniatis"); and by Silhavy, T. J., Bennis, M. L. and Enquist, L. W., Experiments with Gene Fusions, Cold Spring Harbor Laboratory Cold Press Spring Harbor, NY (1984); and by Ausubel, F. M. et al., Current Protocols in Molecular Biology, published by Greene Publishing Assoc. and Wiley-Interscience (1987).

The present invention relates to unique 16S rDNA sequences which have been isolated from the bacteria very similar if not related to *Dehalococcoides ethenogenes*, which are associated with the ability of this bacteria to dechlorinate chlorinated organic compounds. The sequences were isolated from bacteria found in soil samples of various industrial sites that have been shown to contain bacteria that have the ability to dechlorinate chlorinated compounds. The sequences are useful for the identification new dechlorinating bacteria, as well as for sub-typing strains of *Dehalococcoides ethenogenes*.

Dechlorinating bacteria were isolated from the aquifer soil taken from around industrial sites by means well known in the art. Samples were maintained under anaerobic conditions and cultured in a suitable medium for the growth of anaerobic soil bacteria. Such culture procedures and media are common and well known in the art and are described in Manual of Methods for General Bacteriology (Phillipp Gerhardt, R. G. E. Murray, Ralph N. Costilow, Eugene W. Nester, Willis A. Wood, Noel R. Krieg and G. Briggs Phillips, eds), American Society for Microbiology, Washington, DC. (1994)) or by Thomas D. Brock in Biotechnology: A Textbook of Industrial Microbiology, Second Edition, Sinauer Associates, Inc., Sunderland, MA (1989).

In order to enrich the cultured soil samples for dechlorinating bacteria, the samples were contacted with a low level of chlorinated organic compound. A number of chlorinated compounds are suitable for this purpose, including, but not limited to carbontetrachloride, tetrachloroethene, chloroform, dichloromethane, trichloroethene, dichloroethylene, vinyl chloride, and chloroaromatics, where chlorinated ethenes are preferred and TCE and PCE are preferred. Incubation proceeded for about six months, and cultures were analyzed periodically for the disappearance of the chlorinated organic and the appearance of degradation

products. Cultures demonstrating the ability to degrade chlorinated organics, were selected for further analysis.

Bacteria from dechlorinating cultures were removed by standard methods and total chromosomal DNA was isolated from the microorganisms through a bead mill homogenization procedure. A fragment of the 16S rRNA gene was amplified from the genomic DNA extract by PCR using 16S rDNA primers specific for dechlorinating microbes. The 16S rDNA PCR product was cloned and sequenced to confirm its identity (M. I. More et al. 1994. *Appl. Environ. Microbiol.*, 60, 1572-1580). Each raw 16S sequences obtained were assembled into a contig, and a consensus was manually constructed using Seqman II in DNASTar (DNASTar, Inc., Madison, WI). For each test sequence, a Pearson and Lipman similarity search was performed using the FASTA program in GCG (Wisconsin Package Version 9.0, Genetics Computer Group, Madison, WI). The nearest organism in similarity in 16S rRNA sequence to the test sequence was used as the nearest match for identification. Those 16S DNA gene sequences that were identified to be similar to the dechlorinating bacteria, *Dehalococcoides ethenogenes* DHE-195 (GenBank Accession No. AF004928), were aligned with selected 16s rRNA sequences extracted from the Ribosomal Database Project (Michigan State University) that were a representation of the major microorganism domains, Bacteria and Archeae in the Universal Phylogenetic Tree of Life. The sequences were aligned using MegAlign in DNASTar, using the default software parameters. From this alignment probable region for signature sequences were mapped. Then sequences from each region were tested against the Ribosomal Database (RDB) for unique sequences that could be signature sequences and utilized as PCR primes or detection probes.

Within the 16S rDNA profile defined by the comparison of the isolated dechlorinators, (see Figures 1 and 2) three signature regions showed considerable variation from the known sequences. Those regions were defined as extending from E1146 to E1156 (SEQ ID NO:1), from E180 to E227 (SEQ ID NO:8), and from E1001 to E1047 (SEQ ID NO: 30). All of the dechlorinating isolates of the present invention contained the sequence as set forth in SEQ ID NO:1, which is conspicuously absent from the sequence known in the art (Maymó-Gatell et al. (*Science*, 176:1568 (1997)).

Although a region similar to that defined by SEQ ID NO:8 is found in the literature sequence, there are significant variations at positions, E184, E190, E197, E200, E207, E216, and E221 as shown below in Formula I.

Formula I.

E184 E190 E198 E201 E208 E217 E222
 | | | | | | |
 5 TGTGRTGGGCY GACATAWGTY GGTTCAYTAA AGCCGYAAGGYGC TTG (SEQ ID NO:8)

With in the context the present invention Applicants have discovered that within the signature region defined by SEQ ID NO:8 and Formula I above, the R at position E184 may be A/G, the Y at position E190 may be C/T, the W at position E198 may be A/T, and the Y's at position E201, E208, E217, and E222 may be T/C.

Similarly the region defined by SEQ ID NO:30 is also found in the literature but contains significant variations at positions, E1003, E1012, E1020, E1039, and E1040 as shown below in Formula II.

15 Formula II.

E1003 E1012 E1020 E1039
 | | | |
 20 TGWAGTAGTGAACMGAAAGGGRAACGACCTGTTAAGTCAGGARMITGCACA (SEQ ID NO:30)
 |
 E1040

As with SEQ ID NO:8, Applicants have discovered that within the signature region defined by SEQ ID NO:30 and Formula II above, the W at position E1003 may be A/T, at position E1012 the M may be A/C, at position E1020 the R may be A/G, at position E1039 the R may be A/G and , at position E1040 the M may be A/C.

Likewise, if the entire 16S rDNA profile is examined, it is seen that there are significant single base differences throughout the entire profile (Figures 1 and 2). These differences are illustrated in tabular form in Table 2. Accordingly a 16S rDNA profile sequence, having the following bases substitutions taken independently or together will be diagnostic for dechlorinating bacteria: E107=G, base E184=G, base E190=C, E198=T, E201=T, E208=C, E217=T, E222=C, E264=C, E267=C, E291=T, E333=C, E420=C, E444=T, E631=A, E829=A, E933=T, E934=T, E980=C, E1003=T, E1012=T, E1020=G, E1039=A, E1040=C, E1087=T, and E1114=C.

Assay Methods

The instant sequences may be used in a variety of formats for the detection of dechlorinating bacteria. The two most convenient formats will rely on methods

of nucleic acid hybridization or primer directed amplification methods such as PCR.

Nucleic Acid Hybridization Methods

5 The basic components of a nucleic acid hybridization test include a probe, a sample suspected of containing a dechlorinating bacteria and a specific hybridization method. As noted above, probes of the present invention are single strand nucleic acid sequence which is complementary to the nucleic acid sequences to be detected. Probes are "hybridizable" to the nucleic acid sequence to be detected. The probe length can vary from 5 bases to tens of thousands of
10 bases, and will depend upon the specific test to be done. Only part of the probe molecule need be complementary to the nucleic acid sequence to be detected. In addition, the complementarity between the probe and the target sequence need not be perfect. Hybridization does occur between imperfectly complementary molecules with the result that a certain fraction of the bases in the hybridized
15 region are not paired with the proper complementary base. A probe may be composed of either RNA or DNA. The form of the nucleic acid probe may be a marked single strand molecule of just one polarity or marked single strand molecule having both polarities present. The form of the probe, like its length, will be determined by the type of hybridization test to be done.

20 The sample may or may not contain the organism of interest. The sample may take a variety of forms, including liquid such as water, or solid such as dust, or soil. The sample nucleic acid must be made available to contact the probe before any hybridization of probe and target molecule can occur. Thus the organism's RNA must be free from the cell and placed under the proper
25 conditions before hybridization can occur. Methods of in solution hybridization necessitate the purification of the RNA in order to be able to obtain hybridization of the sample rRNA with the probe. This has meant that to utilize the in solution method for detecting target sequences in a sample, the nucleic acids of the sample must first be purified to eliminate protein, lipids, and other cell components, and
30 then contacted with the probe under hybridization conditions. Method for the purification of the sample nucleic acid are common and well known in the art (Maniatis, *supra*).

Similarly, hybridization methods are well defined. Typically the probe and sample must be mixed under conditions which will permit nucleic acid
35 hybridization. This involves contacting the probe and sample in the presence of an inorganic or organic salt under the proper concentration and temperature conditions. The probe and sample nucleic acids must be in contact for a long enough time that any possible hybridization between the probe and sample nucleic

acid may occur. The concentration of probe or target in the mixture will determine the time necessary for hybridization to occur. The higher the probe or target concentration the shorter the hybridization incubation time needed.

In one embodiment, hybridization assays may be conducted directly on bacterial lysates, without the need to extract the nucleic acids. This eliminates several steps from the sample-handling process and speeds up the assay. To perform such assays on crude cell lysates, a chaotropic agent is typically added to the cell lysates prepared as described above. The chaotropic agent stabilizes nucleic acids by inhibiting nuclease activity. Furthermore, the chaotropic agent allows sensitive and stringent hybridization of short oligonucleotide probes to RNA at room temperature [Van Ness and Chen (1991) *Nucl. Acids Res.* 19:5143-5151]. Suitable chaotropic agents include guanidinium chloride, guanidinium thiocyanate, sodium thiocyanate, lithium tetrachloroacetate, sodium perchlorate, rubidium tetrachloroacetate, potassium iodide, and cesium trifluoroacetate, among others. Typically, the chaotropic agent will be present at a final concentration of about 3M. If desired, one can add formamide to the hybridization mixture, typically 30-50% (v/v).

Alternatively, one can purify the rRNA prior to probe hybridization. A variety of methods are known to one of skill in the art (e.g., phenol-chloroform extraction, IsoQuick extraction (MicroProbe Corp., Bothell, WA), and others). Pre-hybridization purification is particularly useful for standard filter hybridization assays. Furthermore, purification facilitates measures to increase the assay sensitivity by incorporating *in vitro* RNA amplification methods such as self-sustained sequence replication (see for example Fahy et al. (1991) in PCR Methods and Applications, Cold Spring Harbor Laboratory Press, pp. 25-33) or reverse transcriptase PCR (Kawasaki (1990) in PCR Protocols: A Guide to Methods and Applications, M. A. Innis et al., eds., pp. 21-27). One can obtain amplified rRNA by using *in vitro* RNA amplification techniques as described in Fahy et al., *supra.*; Kawasaki, *supra.* The exact procedure used is not crucial, provided that it does not amplify significant amounts of DNA, which would tend to obscure results.

Once the pre-rRNA is released from the cells, it can be detected by any of a variety of methods. The method of rRNA detection is not crucial to the invention. However, the most useful embodiments have at least some of characteristics of speed, convenience, sensitivity, and specificity. Direct DNA probe analysis is suitable, as is an *in vitro* RNA amplification method, such as 3SR, that employs labelled primers.

Various hybridization solutions can be employed. Typically, these comprise from about 20 to 60% volume, preferably 30%, of a polar organic solvent. A common hybridization solution employs about 30-50% v/v formamide, about 0.15 to 1M sodium chloride, about 0.05 to 0.1M buffers, such as sodium citrate, Tris-HCl, PIPES or HEPES (pH range about 6-9), about 0.05 to 0.2% detergent, such as sodium dodecylsulfate, or between 0.5-20 mM EDTA, FICOLL (Pharmacia Inc.) (about 300-500 kilodaltons), polyvinylpyrrolidone (about 250-500 kdal), and serum albumin. Also included in the typical hybridization solution will be unlabeled carrier nucleic acids from about 0.1 to 5 mg/mL, fragmented nucleic DNA, e.g., calf thymus or salmon sperm DNA, or yeast RNA, and optionally from about 0.5 to 2% wt./vol. glycine. Other additives may also be included, such as volume exclusion agents which include a variety of polar water-soluble or swellable agents, such as polyethylene glycol, anionic polymers such as polyacrylate or polymethylacrylate, and anionic saccharidic polymers, such as dextran sulfate.

Nucleic acid hybridization is adaptable to a variety of assay formats. One of the most suitable is the sandwich assay format. The sandwich assay is particularly adaptable to hybridization under non-denaturing conditions. A primary component of a sandwich-type assay is a solid support. The solid support has adsorbed to it or covalently coupled to it immobilized nucleic acid probe that is unlabeled and complementary to one portion of the rRNA sequence. Preferred are those probes that hybridize to regions of the rRNA that have minimal secondary and tertiary interactions. The advantage of such probes is that the hybridization can be carried out without the additional step of heat denaturing the sample nucleic acid. For example, the hybridization can be carried out at room temperature.

The sandwich assay may be encompassed in an assay kit. This kit would include a first component for the collection of samples from soil such as vials for containment, and buffers for the disbursement and lysis of the sample. A second component would include media in either dry or liquid form for the hybridization of target and probe polynucleotides, as well as for the removal of undesirable and nonduplexed forms by washing. A third component includes a solid support (dipstick) upon which is fixed or to which is conjugated unlabeled nucleic acid probe(s) that is(are) complementary to a part of the precursor rRNA of the species of bacteria being tested. In the case of multiple target analysis more than one capture probe, each specific for its own rRNA, will be applied to different discrete regions of the dipstick. A fourth component would contain labeled probe that is complementary to a second and different region of the same rRNA strand to

which the immobilized, unlabeled nucleic acid probe of the third component is hybridized.

In another embodiment, the instant 16S rDNA sequence may be used as a 3' blocked detection probe in either a homogeneous or heterogeneous assay format. For example a probe generated from the instant sequences may be 3' blocked or non-participatory and will not be extended by, or participate in, a nucleic acid amplification reaction. Additionally, the probe incorporates a label that can serve as a reactive ligand that acts as a point of attachment for the immobilization of the probe/analyte hybrid or as a reporter to produce detectable signal. Accordingly, genomic or cDNA isolated from the test organism is amplified by standard primer-directed amplification protocols in the presence of an excess of the 16S rDNA 3' blocked detection probe to produce amplification products. Because the probe is 3' blocked, it does not participate or interfere with the amplification of the target. After the final amplification cycle, the detection probe anneals to the relevant portion of the amplified DNA and the annealed complex is then captured on a support through the reactive ligand.

PCR Assay Methods

In an alternate embodiment the present sequences may be used as primers or to generate primers that may be used in primer directed nucleic acid amplification to detect the presence of dechlorinating bacteria. A variety of primer directed nucleic acid amplification methods are known in the art including thermal cycling methods such as polymerase chain reaction (PCR) and ligase chain reaction (LCR) as well as isothermal methods and strand displacement amplification (SDA). The preferred method is PCR. Typically, in PCR-type amplification techniques, the primers have different sequences and are not complementary to each other. Depending on the desired test conditions, the sequences of the primers should be designed to provide for both efficient and faithful replication of the target nucleic acid. Methods of PCR primer design are common and well known in the art. (Thein and Wallace, "The use of oligonucleotide as specific hybridization probes in the Diagnosis of Genetic Disorders", in *Human Genetic Diseases: A Practical Approach*, K. E. Davis Ed., (1986) pp. 33-50 IRL Press, Hemdon, Virginia); Rychlik, W. (1993) In White, B. A. (ed.), *Methods in Molecular Biology*, Vol. 15, pages 31-39, PCR Protocols: Current Methods and Applications. Humana Press, Inc., Totowa, NJ.)

If a nucleic acid target is to be exponentially amplified, then two primers are used each having regions complementary to only one of the strands in the target. After heat denaturation, the single-stranded target fragments bind to the respective primers which are present in excess. Both primers contain asymmetric

restriction enzyme recognition sequences located 5' to the target binding sequences. Each primer-target complex cycles through nicking and polymerization/displacement steps in the presence of a restriction enzyme, a DNA polymerase and the three dNTP's and one dNTP[aS] as discussed above. An in
5 depth discussion of SDA methodology is given by Walker et al., *Proc. Natl. Acad. Sci. U.S.A.*, 89, 392, (1992).

Alternatively, asymmetric amplification can be used to generate the strand complementary to the detection probe. Asymmetric PCR conditions for
10 producing single-stranded DNA would include similar conditions for PCR as described however, the primer concentrations are changed with 50 pmol of the excess primer and 1 pmol of the limiting primer. It is contemplated that this procedure would increase the sensitivity of the method. This improvement in sensitivity would occur by increasing the number of available single strands for binding with the detection probe.

15 Within the context of the present invention primers will be designed to conserved regions of the 16S rDNA profile which are associated with dechlorination. The most significant of those regions are the sequences set forth in SEQ ID NO:1, SEQ ID NO:8 and SEQ ID NO:30.

Following amplification and prior to sequencing, the amplified nucleotide
20 sequence may be ligated to a suitable vector followed by transformation of a suitable host organism with said vector. One thereby ensures a more readily available supply of the amplified sequence. Alternatively, following amplification, the amplified sequence or a portion thereof may be chemically synthesized for use as a nucleotide probe. In either situation the DNA sequence of
25 the variable region is established using methods such as the dideoxy method (Sanger, F. et al. *Proc. Natl. Acad. Sci* (1977) 74, 5463-5467). The sequence obtained is used to guide the choice of the probe for the organism and the most appropriate sequence(s) is/are selected.

EXAMPLES

30 The present invention is further defined in the following Examples. It should be understood that these Examples, while indicating preferred embodiments of the invention, are given by way of illustration only. From the above discussion and these Examples, one skilled in the art can ascertain the essential characteristics of this invention, and without departing from the spirit
35 and scope thereof, can make various changes and modifications of the invention to adapt it to various usages and conditions.

GENERAL METHODS

Standard recombinant DNA and molecular techniques used in the Examples are well known in the art. Techniques suitable for use in the following examples may be found in Sambrook, J., Fritsch, E. F. and Maniatis, T.,
5 Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY (1989) (hereinafter "Maniatis").

Materials and methods suitable for the maintenance and growth of bacterial cultures are well known in the art. Techniques suitable for use in the following examples may be found as set out in Manual of Methods for General
10 Bacteriology (Phillipp Gerhardt, R. G. E. Murray, Ralph N. Costilow, Eugene W. Nester, Willis A. Wood, Noel R. Krieg and G. Briggs Phillips, eds), American Society for Microbiology, Washington, DC. (1994)) or by Thomas D. Brock in Biotechnology: A Textbook of Industrial Microbiology, Second Edition, Sinauer Associates, Inc., Sunderland, MA (1989). All reagents, restriction enzymes and
15 materials used for the growth and maintenance of bacterial cells were obtained from Aldrich Chemicals (Milwaukee, WI), DIFCO Laboratories (Detroit, MI), GIBCO/BRL (Gaithersburg, MD), or Sigma Chemical Company (St. Louis, MO) unless otherwise specified.

Manipulations of genetic sequences were accomplished using the suite of
20 programs available from the Genetics Computer Group Inc. (Wisconsin Package Version 9.0, Genetics Computer Group (GCG), Madison, WI), DNASTAR (DNASTAR, Inc. 1228 S. Park St. Madison, WI 53715 USA), or the "on-line" Probe Match Program from the Ribosomal Database Project II (Michigan State University, East Lansing, MI). Where any sequence analysis software was used in
25 the following examples, default values were used unless otherwise specified.

The meaning of abbreviations is as follows: "h" means hour(s), "min" means minute(s), "sec" means second(s), "d" means day(s), "mL" means milliliters, "L" means liters.

EXAMPLE 1

Isolation And Characterization Of Dechlorinating Soil Organisms

30 Aquifer core samples were obtained by split spoon sampling at depths ranging from 10 to 80 ft, depending on the depth of the particular aquifer to be tested. The cores were taken in sterile stainless steel cylinders or placed in sterile glass vials. The core samples were immediately shipped to the laboratory at
35 ambient temperatures and under anaerobic conditions. Upon arrival the samples were stored in an anaerobic glove bag (chamber) (Coy Laboratory Products Inc., Ann Arbor, MI), whose atmosphere was 10% H₂, 5% CO₂ and 85% N₂.

The laboratory microcosms were prepared in 250 mL Wheaton bottles (Wheaton Co., Millville, NJ) within the anaerobic chamber. Duplicate microcosms were prepared for the following conditions: Killed Control (live soil autoclaved for 1 hr on 2 consecutive days), Live soil, and Live soil + 0.05% yeast extract. Each microcosm contains 20% soil and 80% BTZ-3 media (NH_4Cl , 4.3 g/L; KH_2PO_4 , 50 g/L; $\text{MgCl}\cdot 6\text{H}_2\text{O}$, 20 g/L; $\text{CaCl}_2\cdot 2\text{H}_2\text{O}$, 1 g/L; HEPES, 50 mM/L; mineral solution, 10 mL/L; resazurin 0.2%, 5 mL/L). The microcosms were filled to top such there was little or no headspace, and then stoppered with Teflon™ lined disks and crimp-sealed with aluminum seals (Wheaton Co., Millville, NJ). The resazurin addition permitted the visualization of low potential anaerobic conditions by a color change from pink to colorless. Each microcosm was spiked with 5 ppm from a PCE or TCE solution saturated in water. The microcosms were incubated on their sides in the anaerobic chamber, in the dark, at ambient room temperature (22°C) for up to 180 days.

Samples were analyzed the next day as time zero (t_0) and then twice a week for the dechlorination of PCE or TCE and the formation of cisDCE, vinyl chloride or methane. All samples were taken in the anaerobic chamber by using a syringe mounted with a 23 gauge needle was use to puncture the Teflon™ septa to obtain a 5 mL liquid sample that was injected into a 10 mL headspace vial.

Samples were tested using HP Headspace sampler 7694, HP5890 series II GC (FID detector, HP 5 capillary column #19091J-215), HP3365 Chemstation version A.03.34.

Figure 3 plots the concentration (parts per million; ppm) of chloroethenes in the microcosm medium as a function of time (days) and illustrates the dechlorination of chloroethenes. Dechlorination of PCE to TCE could be detected by GC/FID. Within two days with the formation of cisDCE from the dechlorination of TCE was detected. These results are found in the microcosms that has been amended with 0.05% yeast extract plus minimal salts media (BTZ-3 media). These results can also be seen in the microcosms that are amended with the minimal salts media alone. The difference is the dechlorination is slightly delayed. It takes four days before cisDCE is detected. Degradation of cisDCE would occur over the next two weeks. Vinyl chloride and ethene could only be detected at trace levels. The "Killed" control, did not show degradation of PCE or TCE during the duration of the experiment. Cell growth was shown by increase in the turbidity of the microcosm medium and by microscopic analysis.

EXAMPLE 2

Generation of PCR Primers and Probes for the Amplification and Detection of the *Dehalococcoides Ethenogenes* 16S rRNA Profiled

The detection and sequencing of the *Dehalococcoides ethenogenes*-like organisms used the set of PCR primers are shown in Table 1. The PCR primers were designed using signature sequence regions. To determine the location of these signature sequence, the *Dehalococcoides ethenogenes* sequence (GenBank No. AF004928)[SEQ ID NO:7] was aligned using MEGALIGN (DNASTar, Madison, WI) or Pileup (Genetics Computer Group, Madison, WI) with 16S rRNA sequences from 100 organisms that represent most major domains, families and genera in the major kingdoms of Bacteria and Archaea. The conserved, variable, and highly variable regions could be delineated by boxing off the consensus sequences. Primer candidate sequences were manually picked from the variable and highly variable regions and then their uniqueness was determined by determining their potential as probes to a ribosomal sequence database sequences using the "on-line" Probe Match Program from the Ribosomal Database Project II (<http://www.cme.msu.edu/RDP/html/index.html>) RDPII, Michigan State University, East Lansing, MI). This analysis returned an overview of the matches between a probe and its potential target sequence, as a listing and as a phylogenetic overview. The program results showed the sequences that match the query sequence (if there are such sequences) and also showed sequences that had mismatches, deletions and insertions, citing the number and positions of the aberrations.

The sequences which were unique and passed this test as signature sequences were then designed as either a forward or reverse primer, usually dependent on their position in the sequence. The most unique sequence of the signature sequence (specificity) was designed into the 3' end in either type of primer. The selected primers are shown in Table 1.

The primers were synthesized using standard β -cyanoethyl phosphoramidite coupling chemistry on controlled pore glass (CPG) supports on automated DNA oligonucleotide synthesizer (Applied Biosystems Model 392, Perkin-Elmer, Foster City, CA)

The primers were tested after they were synthesized using PCR on samples taken from microcosms known to have *Dehalococcoides ethenogenes*-like organisms. The PCR products were sized on agarose electrophoresis and then cloned and sequenced to verify that the amplified sequences were *Dehalococcoides ethenogenes*-like 16S rRNA sequences.

TABLE 1Primers for *Dehalococcoides ethenogenes*

FP DHE 32	5'AAG TCGAACGGTCTTAAGCA3' SEQ ID NO:9
RP DHE422	5' CGTCATTATTCTTCCCTGTG 3' SEQ ID NO:10
FP DHE 958	5'GGGAAACGACCTGTTAAGTCA 3' SEQ ID NO:11
RP DHE 1212	5'GGATTAGCTCCAGTTCACACTG 3' SEQ ID NO:12
RP DHE 1076	5'AAATTTAACTAGCAACAAGG 3' SEQ ID NO:13
FP DHE 795	5'GGAGTATCGACCCTCTCTG 3' SEQ ID NO:14
FP DHE 774	5'GGGAGTATCGACCCTCTC 3' SEQ ID NO:15
FP DHE 946	5'AGTGAACCGAAAGGGAAA 3' SEQ ID NO:16
FP DHE 385	5'GGGTTGTAAACCTCTTTTCAC 3' SEQ ID NO:17
RP DHE 806	5'GTTAGCTTCGGCACAGAGAG 3' SEQ ID NO:18
RP DHE 692	5'TCAGTGACAACCTAGAAAAC 3' SEQ ID NO:19
FP DHE1	5'GATGAACGCTAGCGGCG 3' SEQ ID NO:20
FP DHE 30	5'GTGCCTTATGCATGCAAG 3' SEQ ID NO:21
FP DHE 1187	5' AATAGGTTGCAACAGTGTGAA 3' SEQ ID NO:22
FP DHE 1175	5' AATGGACAGAACAATAGGTTGC 3' SEQ ID NO:23
RP DHE 1381	5' GGCACATCGACTTCAAGTGTT 3' SEQ ID NO:24
RP DHE 1381	5' GGCACATCGACTTCAAGTGTT 3' SEQ ID NO:25
FP DHE 558	5' TAACCGGGACG(AT)GTCATTCA 3' SEQ ID NO:26
FP DHE 593	5' GAGTACAGCAGGAGAAAAC 3' SEQ ID NO:27
RP DHE 1394	5' CCTCCTTGCGGTTGGCACATC 3' SEQ ID NO:28
RP DHE 1090	5' GGCAGTCTCGCTAGAAAAT 3' SEQ ID NO:29

EXAMPLE 3

5 Using the *Dehalococcoides Ethenogenes*-Like Specific Primers
 to Detect These Organisms in Microcosms

10 Nucleic acids were extracted from the microcosm cultures by a bead mill
 homogenization procedure, FastDNA Spin Kit for Soil (Bio 101, Vista, CA), that
 was designed to isolate genomic DNA from all cell types. Approximately 10 mL
 of the microcosm culture was pelleted and resuspended in 500 ul of the culture
 media. The resuspended pellet was added to a 2.2 mL conical screw-cap tube
 containing 1.5 g of three differently sized glass and zirconia/silica beads
 (106 microns, 710-1180 microns). To the sample tubes, 978 ul of sodium
 phosphate buffer and 122 ul of MT buffer was added. The tubes were
 15 homogenized for 30 seconds at speed 5.5 on a Fast Prep bead mill homogenizer.
 A clear supernatant was obtained by centrifuging the samples at 14,000 x g for
 30 seconds. The supernatant was transferred to a clean microcentrifuge tube and

250 μ l of PPS reagent was added and mixed. The resulting precipitate was pelleted through centrifugation at 14,000 x g for 5 minutes. The supernatant was transferred to a new microcentrifuge tube and 1 mL of binding matrix was added. The samples were placed on a rotator for 2 minutes and then sat on the benchtop for 3 minutes to allow the settling of the silica matrix. Between 500-700 μ l of the supernatant was removed and discarded. The remaining supernatant was used to resuspend the silica matrix and transferred to a spin filter. The spin filter was centrifuged for 1 minute at 14,000 x g and the flow-through decanted. The silica matrix was washed with 500 μ l of SEWS-M buffer and centrifuged for 1 minute at 16,000 x g. The flow through was discarded and any residual buffer in the matrix was removed by a 2 minute centrifugation at 14,000 x g. The spin filter was placed in a catch tube and air dried for 5 minutes in a biological hood. The genomic DNA was eluted by adding 60 μ l of sterile, deionized water, mixing the matrix and the water together with a pipet tip, and centrifuging for 1 minute at 14,000 x g.

The 16S rRNA gene for *Dehalococcoides ethenogenes* was detected by PCR amplification and gel electrophoresis. The 16S sequences were amplified using *Dehalococcoides ethenogenes* specific 16S rDNA primers shown in Table 1. All PCR amplifications were performed using the GeneAmp PCR kit with Taq DNA polymerase (PE Applied Biosystems, Branchburg, NJ) in a Perkin Elmer 9600 thermal cycler. Amplification reactions contained 10 mM Tris-HCl (pH 8.3), 50 mM KCl, 1.5 mM $MgCl_2$, 10 μ M each deoxynucleoside triphosphate, 20 pmol each primer, 2.5 U of Taq polymerase, and 1 μ L of the genomic extraction diluted 1:10 in a final reaction volume of 50 μ L. The PCR conditions were as follows: 2 minutes of denaturation at 95 $^{\circ}$ C, followed by 30 cycles of 30 seconds at 94 $^{\circ}$ C, 30 seconds at 55 $^{\circ}$ C, 30 seconds at 72 $^{\circ}$ C. 8 μ L of the PCR product was visualized on a 2% agarose gel (SeaKem GTG, FMC BioProducts, Rockland, ME) stained with ethidium bromide.

A direct detection protocol used 1 μ L of the microcosm culture was directly added to the PCR as described previously.

After the *Dehalococcoides ethenogenes*-like sequences were detected in the microcosm developed from contaminated soil, FP DHE 1 (SEQ ID NO:20), RP DHE 1330 (SEQ ID NO:12) were used to amplify a 1212 bp (or 1221 bp) fragment, which was cloned (using the PCR dA/T-Cloning System, Invitrogen, Inc., CA) and sequenced (using Model 377 DNA Sequencer kit and system, Applied Biosystems, Perkin-Elmer, Foster City, CA). The sequence was assembled using the Seqman II program (DNASTar, Inc., Madison, WI). The 16S rDNA sequence contig formed was compared to 16S rDNA sequences obtained

from microcosms developed from contaminated soils from other sites and the comparison is shown in Figure 4.

Figure 4 shows a gel of amplification products generated from PCR amplification of various *Dehalococcoides ethenogenes* isolated from a number of industrial sites contaminated with either PCE or TCE. All amplifications were carried out using primers SEQ ID NOs:17 paired with 19, and SEQ ID NOs:18 paired with 20. Lanes 1 and 12 carry the molecular weight markers. Lanes 2 and 3 are the PCR products generated from organisms isolated from soil containing PCE. Lanes 4, 5, 6, 7, 8 and 9 are the PCR products from organisms isolated from soil containing TCE. Lanes 10 and 11 contain negative PCR controls. As can be seen by the data all samples were detectable by the primers used.

The contiguous sequences from each site was unique, having 96 to 99% similarity to each other. The differences in the sequence are annotated in Table 2. A major difference exists in the consensus sequence that were obtained from all strains (CS) detected at contaminated sites and the reference sequence represented by the published sequence from strain DHE-195 strain (Table 2). At DHE (CS) positions 1088-1096 (*E. coli* coordinates E1146-E1156) there exists a nine base deletion. The sequence in CS strains reads ATTTTCTAGCGAGACTG (SEQ ID NO:31); in the DHE-195 strain it reads ATTTTCTAGCGAGACTAGCGAGACTG (SEQ ID NO:32) (the double underlined sequence is the sequence deleted in the CS strain sequences. Differences in sequence were found at six other base positions as shown below in Table 2.

TABLE 2

<i>E. coli</i>	DHE No.	DHE-195	DHE-PL	DHE-STF	DHE-DAB	DHE PIN	DHE DLL
28	1	1	1	1	1	1	1
107	66	A	A	A	G	G	A
184	144	A	A	G	G	G	G
190	150	T	T	C	C	C	C
198	157	A	A	A	T	T	A
201	160	C	C	T	T	T	T
208	167	T	T	C	C	C	C
217	176	C	C	T	T	T	T
222	181	T	T	T	C	C	T
264	226	T	T	C	T	T	C
267	*229	T	C	C	C	C	C
291+	254	d	d	T	d	d	d
333	*296	G	C	C	C	C	C
420	383	T	T	C	T	T	C
444	407	C	C	C	T	T	C

<i>E. coli</i>	DHE No.	DHE-195	DHE-PL	DHE-STF	DHE-DAB	DHE-PIN	DHE-DLL
542	*481	G 480	d 479+	d 480+	d 479+	d 479+	d 479+
631	571	T 570	T 569	T 570	A 569	A 569	T 569
829	769	G 768	G 767	A 768	G 767	G 767	
933	874	G 873	T 872	G 873	G 872	G 872	G 872
934	875	C 874	T 873	C 874	C 873	C 873	C 873
980	*921	d 919+	C 919	C 920	C 919	C 919	C 919
1003	944	A 942	A 942	A 943	T 942	T 942	A 942
1012	955	C 953	C 953	C 954	T 953	T 953	C 953
1020	963	A 961	A 961	A 962	G 961	G 961	A 961
1039	984	G 982	G 982	G 983	A 982	A 982	G 982
1040	985	T 983	T 983	T 984	C 983	C 983	T 983
1087	*1033	G 103	T 1031	T 1032	T 1031	T 1031	T 1031
1114	*1060	d 1057+	C 1058	C 1059	C 1058	C 1058	C 1058
1144-56	1088-96	1086-94 ACTAGC	d 1085+	d 1086+	d 1085+	d 1085+	d 1085+

Legend: DHE No. = Consensus number; number (+) = last base coordinate before base a deletion; bold (red) bases are indicative of base sequences different from DHE 195; (*), bold bases and blocks cells (base and coordinate) implies sequence of all 16S sequences isolates that are different from DHE 195

What is Claimed is:

1. An isolated 16S rDNA sequence indicative of a dechlorinating bacterial strain selected from the group consisting of:

- 5 (a) SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6 SEQ ID NO:8 and SEQ ID NO:30;
- (b) an isolated nucleic acid molecule that hybridizes with (a) under the following hybridization conditions: 0.1X SSC, 0.1% SDS at 65°C; and
- (c) an isolated nucleic acid molecule that is completely complementary to (a) or (b).

10 2. An isolated 16S rDNA sequence indicative of a dechlorinating bacterial strain selected from the group consisting of:

- (a) SEQ ID NOs:9-29;
- (b) an isolated nucleic acid molecule that hybridizes with (a) under the following hybridization conditions: 0.1X SSC, 0.1% SDS at 65°C; and
- 15 (c) an isolated nucleic acid molecule that is completely complementary to (a) or (b).

3. An isolated 16S rDNA sequence of Claim 1 wherein within the 16S DNA sequence the following bases, taken independently or together are:

20 base E107=G, base E184=G, base E190=C, E 198=T, E201= T, E208=C, E217=T, E222=C, E264=C, E267=C, E291=T, E333= C, E420=C, E444=T, E631=A, E829=A, E933=T, E934=T, E980=C, E1003=T, E1012=T, E1020=G, E1039=A, E1040=C, E1087=T, and E1114=C.

4. An isolated 16S rDNA sequence indicative of a dechlorinating bacterial strain as set forth in SEQ ID NO:1.

25 5. An isolated bacterial strain comprising any one of the sequences of Claims 1, 3 or 4 wherein said strain has the ability to dechlorinate chlorinated compounds.

6. A method for identifying a dechlorinating bacterial strain comprising:

- 30 (i) extracting genomic DNA from a cell suspected of being able to dechlorinate chlorinated compounds;
- (ii) probing the extracted genomic DNA with a probe derived from any one of the sequences of Claims 1, 2, 3 or 4 under suitable hybridization conditions;

wherein the identification of a hybridizable nucleic acid fragment confirms the presence of a bacteria capable of dechlorinating chlorinated compounds.

35 7. A method for identifying a dechlorinating bacterial strain comprising:

- (i) extracting genomic DNA from a cell suspected of being able to dechlorinate chlorinated compounds; and

- (ii) amplifying the extracted genomic DNA with at least one oligonucleotide primer corresponding to a portion of any one of the sequences of Claims 1, 2, 3 or 4 such that amplification products are generated;

5 wherein the presence of amplification products confirms the presence of a bacteria capable of dechlorinating chlorinated compounds.

8. A method for the dechlorination of chlorinated compounds comprising contacting a chlorinated compound with the isolated bacterial strain of Claim 5 under conditions for the dechlorination to occur.

10 9. A method according to Claim 8 wherein said dechlorinating compound is selected from the group consisting of carbontetrachloride, tetrachloroethene, chloroform, dichloromethane, trichloroethene, dichloroethylene, vinyl chloride, and chloroaromatics.

1/17

FIG. 1-1

DHE seq alignments1.msf MSF: 1223

Name: Deh_eth._.(cornell)

Name: Deh_eth._.(stf)

Name: Dehal_eth._.(pl)._seq

Name: Dehlo_eth._.(dll)..seq

Name: Dehlo_eth._.(dab).

Name: Dehlo_eth._.(pin).seq

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1
Deh_eth._.(cornell)
Deh_eth._.(stf)
Dehal_eth._.(pl)._seq
Dehlo_eth._.(dll)..seq
Dehlo_eth._.(dab).seq
Dehlo_eth._.(pin).seq
60
GATGAACGCTAGCGGCGTGCCCTTATGCAATGCAAGTCGAACGGTCTTTAAGCAATTAAAGATA
GATGAACGCTAGCGGCGTGCCCTTATGCAATGCAAGTCGAACGGTCTTTAAGCAATTAAAGATA
GATGAACGCTAGCGGCGTGCCCTTATGCAATGCAAGTCGAACGGTCTTTAAGCAATTAAAGATA
GATGAACGCTAGCGGCGTGCCCTTATGCAATGCAAGTCGAACGGTCTTTAAGCAATTAAAGATA
GATGAACGCTAGCGGCGTGCCCTTATGCAATGCAAGTCGAACGGTCTTTAAGCAATTAAAGATA
GATGAACGCTAGCGGCGTGCCCTTATGCAATGCAAGTCGAACGGTCTTTAAGCAATTAAAGATA
GATGAACGCTAGCGGCGTGCCCTTATGCAATGCAAGTCGAACGGTCTTTAAGCAATTAAAGATA

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61
Deh_eth._.(cornell)
Deh_eth._.(stf)
Dehal_eth._.(pl)._seq
Dehlo_eth._.(dll)..seq
Dehlo_eth._.(dab).seq
Dehlo_eth._.(pin).seq
120
GTGGCAACCGGTGAGTAACGCGTAAGTAACCTACCTAAGTGGGGGATAGCTTCGGGA
GTGGCAACCGGTGAGTAACGCGTAAGTAACCTACCTAAGTGGGGGATAGCTTCGGGA
GTGGCAACCGGTGAGTAACGCGTAAGTAACCTACCTAAGTGGGGGATAGCTTCGGGA
GTGGCAACCGGTGAGTAACGCGTAAGTAACCTACCTAAGTGGGGGATAGCTTCGGGA
GTGGCAACCGGTGAGTAACGCGTAAGTAACCTACCTAAGTGGGGGATAGCTTCGGGA
GTGGCAACCGGTGAGTAACGCGTAAGTAACCTACCTAAGTGGGGGATAGCTTCGGGA
GTGGCAACCGGTGAGTAACGCGTAAGTAACCTACCTAAGTGGGGGATAGCTTCGGGA

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121
Deh_eth._.(cornell)
Deh_eth._.(stf)
Dehal_eth._.(pl)._seq
Dehlo_eth._.(dll)..seq
Dehlo_eth._.(dab).seq
Dehlo_eth._.(pin).seq
180
AACTGAAGGTAATACCGCATGTGATGGGCTGACATAAGTCGGTTCATTAAAGCCGCAAGG
AACTGAAGGTAATACCGCATGTGATGGGCTGACATAAGTCGGTTCATTAAAGCCGTAAGG
AACTGAAGGTAATACCGCATGTGATGGGCTGACATAAGTCGGTTCATTAAAGCCGCAAGG
AACTGAAGGTAATACCGCATGTGATGGGCTGACATAAGTCGGTTCATTAAAGCCGTAAGG
AACTGAAGGTAATACCGCATGTGATGGGCTGACATAAGTCGGTTCATTAAAGCCGTAAGG
AACTGAAGGTAATACCGCATGTGATGGGCTGACATAAGTCGGTTCATTAAAGCCGTAAGG
AACTGAAGGTAATACCGCATGTGATGGGCTGACATAAGTCGGTTCATTAAAGCCGTAAGG

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Deh_eth._.(cornell)	TCGATCGGTAGCT.GGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGGCCAG	300
Deh_eth._.(stf)	TCGATCGGTAGCTTGGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGGCCAG	
Dehal._eth._.(pl)._seq	TCGATCGGTAGCT.GGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGGCCAG	
Dehlo._eth._.(dll)._seq	TCGATCGGTAGCT.GGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGGCCAG	
Dehlo._eth._.(dab)._seq	TCGATCGGTAGCT.GGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGGCCAG	
Dehlo._eth._.(pin)._seq	TCGATCGGTAGCT.GGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACACGGGCCAG	

Deh_eth._.(cornell)	ACTCCTACGGAGGCAGCAAGGAATCTTGGCAATGGCGAAAGCCTGACCCAGCAA	360
Deh_eth._.(stf)	ACTCCTACGGAGGCAGCAAGGAATCTTGGCAATGGCGAAAGCCTGACCCAGCAA	
Dehal._eth._(pl)._seq	ACTCCTACGGAGGCAGCAAGGAATCTTGGCAATGGCGAAAGCCTGACCCAGCAA	
Dehlo._eth._(dll)._seq	ACTCCTACGGAGGCAGCAAGGAATCTTGGCAATGGCGAAAGCCTGACCCAGCAA	
Dehlo._eth._(dab)._seq	ACTCCTACGGAGGCAGCAAGGAATCTTGGCAATGGCGAAAGCCTGACCCAGCAA	
Dehlo._eth._(pin)._seq	ACTCCTACGGAGGCAGCAAGGAATCTTGGCAATGGCGAAAGCCTGACCCAGCAA	

Deh_eth._.(cornell)	CGCCGCGTGAGGGATGAAGGCTTTCGGGTTGTAAACCTCTTTTCACAGGGAAGATAATG	420
Deh_eth._.(stf)	CGCCGCGTGAGGGATGAAGGCTCTCGGGTTGTAAACCTCTTTTCACAGGGAAGATAATG	
Dehal._eth._(pl)._seq	CGCCGCGTGAGGGATGAAGGCTTTCGGGTTGTAAACCTCTTTTCACAGGGAAGATAATG	
Dehlo._eth._(dll)._seq	CGCCGCGTGAGGGATGAAGGCTCTCGGGTTGTAAACCTCTTTTCACAGGGAAGATAATG	
Dehlo._eth._(dab)._seq	CGCCGCGTGAGGGATGAAGGCTTTCGGGTTGTAAACCTCTTTTCACAGGGAAGATAATG	
Dehlo._eth._(pin)._seq	CGCCGCGTGAGGGATGAAGGCTTTCGGGTTGTAAACCTCTTTTCACAGGGAAGATAATG	


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Deh_eth._.(cornell)
Deh_eth._.(stf)
Dehal._eth._(pl)._seq
Dehlo._eth._(dll)._seq
Dehlo._eth._(dab)._seq
Dehlo._eth._(pin)._seq

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Deh_eth._ (cornell)	GCAGGAGAAAACGGAAATTC	CCGGTGTAGTGGTAAAAAT	GCGTAGATATCGGAGGAACACC
Deh_eth._ (stf)	GCAGGAGAAAACGGAAATTC	CCGGTGTAGTGGTAAAAAT	GCGAGGAACACC
Dehal._eth._ (pl) . _seq	GCAGGAGAAAACGGAAATTC	CCGGTGTAGTGGTAAAAAT	GCGGAGGAACACC
Dehlo._eth._ (dll) . _seq	GCAGGAGAAAACGGAAATTC	CCGGTGTAGTGGTAAAAAT	GCGGAGGAACACC
Dehlo._eth._ (dab) . _seq	GCAGGAGAAAACGGAAATTC	CCGGTGTAGTGGTAAAAAT	GCGGAGGAACACC
Dehlo._eth._ (pin) . _seq	GCAGGAGAAAACGGAAATTC	CCGGTGTAGTGGTAAAAAT	GCGGAGGAACACC

4/17

FIG. 1-4

661
 Deh_eth._.(cornell) 720
 Deh_eth._.(stf)
 Dehal_eth._(pl)..seq
 Dehlo_eth._(dll)..seq
 Dehlo_eth._(dab).seq
 Dehlo_eth._(pin).seq

721
 Deh_eth._.(cornell) 780
 Deh_eth._.(stf)
 Dehal_eth._(pl)..seq
 Dehlo_eth._(dll)..seq
 Dehlo_eth._(dab).seq
 Dehlo_eth._(pin).seq

781
 Deh_eth._.(cornell) 840
 Deh_eth._.(stf)
 Dehal_eth._(pl)..seq
 Dehlo_eth._(dll)..seq
 Dehlo_eth._(dab).seq
 Dehlo_eth._(pin).seq

841
 Deh_eth._.(cornell) 900
 Deh_eth._.(stf)
 Dehal_eth._(pl)..seq
 Dehlo_eth._(dll)..seq
 Dehlo_eth._(dab).seq
 Dehlo_eth._(pin).seq

FIG. 1-5

960

1020

0807

1140

6/17

FIG. 1-6

1141
Deh_eth._.(cornell) 1200
Deh_eth._.(stf) AGCATGGCCCTTTATATCTTTGGGCTACACACGCTACAATGGACAGAACAAATAGGTTGCA
Dehal._eth._.(pl)..seq AGCATGGCCCTTTATATCTTTGGGCTACACACGCTACAATGGACAGAACAAATAGGTTGCA
Dehlo._eth._.(dll)..seq AGCATGGCCCTTTATATCTTTGGGCTACACACGCTACAATGGACAGAACAAATAGGTTGCA
Dehlo._eth._.(dab)..seq AGCATGGCCCTTTATATCTTTGGGCTACACACGCTACAATGGACAGAACAAATAGGTTGCA
Dehlo._eth._.(pin)..seq AGCATGGCCCTTTATATCTTTGGGCTACACACGCTACAATGGACAGAACAAATAGGTTGCA

1201
Deh_eth._.(cornell) 1223
Deh_eth._.(stf) ACAGTGTGAACTGGAGCTAATCC Seq. I.D. No. 7
Dehal._eth._.(pl)..seq ACAGTGTGAACTGGAGCTAATCC Seq. I.D. No. 3
Dehlo._eth._.(dll)..seq ACAGTGTGAACTGGAGCTAATCC Seq. I.D. No. 2
Dehlo._eth._.(dab)..seq ACAGTGTGAACTGGAGCTAATCC Seq. I.D. No. 6
Dehlo._eth._.(pin)..seq ACAGTGTGAACTGGAGCTAATCC Seq. I.D. No. 4
Dehlo._eth._.(pin)..seq ACAGTGTGAACTGGAGCTAATCC Seq. I.D. No. 5

FIG. 2-1

```

12/10/98BEAlignmentG.msf MSF: 1576
Name: E.coli.rnaB Len: 1542
Name: Deh_eth._(cornell) Len: 1443 DHE-195
Name: Deh_eth._(stf) Len: 1212 STFD
Name: Dehal._eth._(pl)._seq Len: 1212
Name: Dehlo._eth.(dab).seq Len: 1212
Name: Dehlo._eth.(pin).seq Len: 1212
Name: Dehlo._eth.(dll).seq Len: 1212
//
1
E.coli.rnaB AAATTGAAGAGTTTGATCATGGCTCAGATTGAACGCTGGCGGCAGGCCCTAACACATGCAA 60
Deh_eth._(cornell) ..... GATGAACGCTAGCGCGTGCCTTATGCATGCAA
Deh_eth._(stf) ..... GATGAACGCTAGCGCGTGCCTTATGCATGCAA
Dehal._eth._(pl)._seq ..... GATGAACGCTAGCGCGTGCCTTATGCATGCAA
Dehlo._eth.(dab).seq ..... GATGAACGCTAGCGCGTGCCTTATGCATGCAA
Dehlo._eth.(pin).seq ..... GATGAACGCTAGCGCGTGCCTTATGCATGCAA
Dehlo._eth.(dll).seq ..... GATGAACGCTAGCGCGTGCCTTATGCATGCAA
61
E.coli.rnaB GTCGAACGGTAACAGGAAGAAGCTTGCTTCTGTACGAGTGGCGACGGGTGAGTAA
Deh_eth._(cornell) GTCGAACGGTCTTAAGCAA... TTAA..... GAT.AGTGGCAACGGGTGAGTAA
Deh_eth._(stf) GTCGAACGGTCTTAAGCAA... TTAA..... GAT.AGTGGCAACGGGTGAGTAA
Dehal._eth._(pl)._seq GTCGAACGGTCTTAAGCAA... TTAA..... GAT.AGTGGCAACGGGTGAGTAA
Dehlo._eth.(dab).seq GTCGAACGGTCTTAAGCAA... TTAA..... GAT.AGTGGCAACGGGTGAGTAA
Dehlo._eth.(pin).seq GTCGAACGGTCTTAAGCAA... TTAA..... GAT.AGTGGCAACGGGTGAGTAA
Dehlo._eth.(dll).seq GTCGAACGGTCTTAAGCAA... TTAA..... GAT.AGTGGCAACGGGTGAGTAA

```

FIG. 2-3

WO 00/63443

PCT/US00/09883

9/17

296 E.coli.rnaB 355
Deh_eth._.(cornell) TGAGAGGATGACCAGCCACACTGGAACCTGAGACACGGTCCAGACTCCTACGGGAGGCAGC
Deh_eth._.(stf) TGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCCAGACTCCTACGGGAGGCAGC
Dehal._eth._.(pl)._seq TGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCCAGACTCCTACGGGAGGCAGC
Dehlo._eth._.(dab).seq TGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCCAGACTCCTACGGGAGGCAGC
Dehlo._eth._.(pin).seq TGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCCAGACTCCTACGGGAGGCAGC
Dehlo._eth._.(dll).seq TGAGAGGATGATCAGCCACACTGGGACTGAGACACGGCCAGACTCCTACGGGAGGCAGC

356 E.coli.rnaB 415
Deh_eth._.(cornell) AGTGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCGCGTGTATGAAGAA
Deh_eth._.(stf) AGCAAGGAATCTTGGCAATGGGCAATGGGCAAGCCTGACCCAGCAACGCCGCGTGAGGGATGAA
Dehal._eth._.(pl)._seq AGCAAGGAATCTTGGCAATGGGCAATGGGCAAGCCTGACCCAGCAACGCCGCGTGAGGGATGAA
Dehlo._eth._.(dab).seq AGCAAGGAATCTTGGCAATGGGCAATGGGCAAGCCTGACCCAGCAACGCCGCGTGAGGGATGAA
Dehlo._eth._.(pin).seq AGCAAGGAATCTTGGCAATGGGCAATGGGCAAGCCTGACCCAGCAACGCCGCGTGAGGGATGAA
Dehlo._eth._.(dll).seq AGCAAGGAATCTTGGCAATGGGCAATGGGCAAGCCTGACCCAGCAACGCCGCGTGAGGGATGAA

416 E.coli.rnaB 475
Deh_eth._.(cornell) GGCCTTCGGGTTGTAAAGTACTTTCAGCGGGAGGAAGGAGTAAGTTAATACCTTTGC
Deh_eth._.(stf) GGCCTTCGGGTTGTAAACCTCTTTTCACAGGGAAGAA.....TAAT.....
Dehal._eth._.(pl)._seq GGCCTTCGGGTTGTAAACCTCTTTTCACAGGGAAGAA.....TAAT.....
Dehlo._eth._.(dab).seq GGCCTTCGGGTTGTAAACCTCTTTTCACAGGGAAGAA.....TAAT.....
Dehlo._eth._.(pin).seq GGCCTTCGGGTTGTAAACCTCTTTTCACAGGGAAGAA.....TAAT.....
Dehlo._eth._.(dll).seq GGCCTTCGGGTTGTAAACCTCTTTTCACAGGGAAGAA.....TAAT.....

FIG. 2-2

121 179
 E.coli.rnaB TGTCTGGGAAC.TGCCTGATGGAGGGGATAACTACTGGAACGGTAGCTAATACCGCA
 Deh_eth._.(cornell) CGCGTAAGTAACCTACCTCTAAGTGGGGATAGCTTCGGGAACTGAAGGTAATACCGCA
 Deh_eth._.(stf) CGCGTAAGTAACCTACCTCTAAGTGGGGATAGCTTCGGGAACTGAAGGTAATACCGCA
 Dehal._eth._.(pl).seq CGCGTAAGTAACCTACCTCTAAGTGGGGATAGCTTCGGGAACTGAAGGTAATACCGCA
 Dehlo._eth._.(dab).seq CGCGTAAGTAACCTACCTCTAAGTGGGGATAGCTTCGGGAACTGAAGGTAATACCGCA
 Dehlo._eth._.(pin).seq CGCGTAAGTAACCTACCTCTAAGTGGGGATAGCTTCGGGAACTGAAGGTAATACCGCA
 Dehlo._eth._.(dll).seq CGCGTAAGTAACCTACCTCTAAGTGGGGATAGCTTCGGGAACTGAAGGTAATACCGCA

180 236
 E.coli.rnaB TAACGTCGCAAGACCAAGAGGGGACCTTCGGCCCTCTTGCCATCGGATGTG...CCCA
 Deh_eth._.(cornell) TGTGATGGGCTGAC.ATAAGTCGGTTCAATAAGCCGCAAGGTGCTTGGTGAGGGGCTTG
 Deh_eth._.(stf) TGTGGTGGGCCGAC.ATAAGTTGGTTCACATAAGCCGTAAGGTGCTTGGTGAGGGGCTTG
 Dehal._eth._.(pl).seq TGTGATGGGCTGAC.ATAAGTCGGTTCAATAAGCCGCAAGGTGCTTGGTGAGGGGCTTG
 Dehlo._eth._.(dab).seq TGTGGTGGGCCGAC.ATATGTTGGTTCACATAAGCCGTAAGGGCGCTTGGTGAGGGGCTTG
 Dehlo._eth._.(pin).seq TGTGGTGGGCCGAC.ATATGTTGGTTCACATAAGCCGTAAGGGCGCTTGGTGAGGGGCTTG
 Dehlo._eth._.(dll).seq TGTGGTGGGCCGAC.ATAAGTTGGTTCACATAAGCCGTAAGGTGCTTGGTGAGGGGCTTG

237 295
 E.coli.rnaB GATGGGATTAGCTAGTAGTGGGGTAACGGCTCACCTAGGCGACGATCCCTAGCT.GGTC
 Deh_eth._.(cornell) CGTCCGATTAGCTAGTTGGTGGGGTAATGGTCTACCAAGGCTTCGATCGGTAGCT.GGTC
 Deh_eth._.(stf) CGTCCGATTAGCTAGTTGGTGGGGTAACGGCTCACCAAGGCTTCGATCGGTAGCTTGGTC
 Dehal._eth._.(pl).seq CGTCCGATTAGCTAGTTGGTGGGGTAATGGCTACCAAGGCTTCGATCGGTAGCT.GGTC
 Dehlo._eth._.(dab).seq CGTCCGATTAGCTAGTTGGTGGGGTAATGGCTACCAAGGCTTCGATCGGTAGCT.GGTC
 Dehlo._eth._.(pin).seq CGTCCGATTAGCTAGTTGGTGGGGTAATGGCTACCAAGGCTTCGATCGGTAGCT.GGTC
 Dehlo._eth._.(dll).seq CGTCCGATTAGCTAGTTGGTGGGGTAACGGCTCACCAAGGCTTCGATCGGTAGCT.GGTC

FIG. 2-2

121
 E.coli.rnab 179
 Deh_eth._(cornell) TGTCTGGGAAC.TGCCTGATGGAGGGGATAACTACTGGAACGGTAGCTAATACCGCA
 Deh_eth._(stf) CGCGTAAGTAACCTACCTCTAAGTGGGGATAGCTTCGGGAACTGAAGGTAATACCGCA
 Dehal._eth._(pl).seq CGCGTAAGTAACCTACCTCTAAGTGGGGATAGCTTCGGGAACTGAAGGTAATACCGCA
 Dehlo._eth._(dab).seq CGCGTAAGTAACCTACCTCTAAGTGGGGATAGCTTCGGGAACTGAAGGTAATACCGCA
 Dehlo._eth._(pin).seq CGCGTAAGTAACCTACCTCTAAGTGGGGATAGCTTCGGGAACTGAAGGTAATACCGCA
 Dehlo._eth._(dll).seq CGCGTAAGTAACCTACCTCTAAGTGGGGATAGCTTCGGGAACTGAAGGTAATACCGCA

180
 E.coli.rnab 236
 Deh_eth._(cornell) TGTGATGGGCTGAC.ATAAGTCGGTTCAATAAGCCGCAAGGTGCTTGGTACCGGATGTG...CCCA
 Deh_eth._(stf) TGTGGTGGGCCGAC.ATAAGTTGGTTCACCTAAAGCCGTAAGGTGCTTGGTGAGGGCTTG
 Dehal._eth._(pl).seq TGTGATGGGCTGAC.ATAAGTCGGTTCAATAAGCCGCAAGGTGCTTGGTGAGGGCTTG
 Dehlo._eth._(dab).seq TGTGGTGGGCCGAC.ATATGTTGGTTCACCTAAAGCCGTAAGCGCTTGGTGAGGGCTTG
 Dehlo._eth._(pin).seq TGTGGTGGGCCGAC.ATATGTTGGTTCACCTAAAGCCGTAAGCGCTTGGTGAGGGCTTG
 Dehlo._eth._(dll).seq TGTGGTGGGCCGAC.ATAAGTTGGTTCACCTAAAGCCGTAAGGTGCTTGGTGAGGGCTTG

237
 E.coli.rnab 295
 Deh_eth._(cornell) GATGGATTAGCTAGTAGGTGGGTAACGGCTCACCTAGCGGACCATCCCTAGCT.GGTC
 Deh_eth._(stf) CGTCCGATTAGCTAGTTGGTGGGGTAATGGTCTACCAAGGCTTCGATCGGTAGCT.GGTC
 Dehal._eth._(pl).seq CGTCCGATTAGCTAGTTGGTGGGGTAATGGCTACCAAGGCTTCGATCGGTAGCT.GGTC
 Dehlo._eth._(dab).seq CGTCCGATTAGCTAGTTGGTGGGGTAATGGCTACCAAGGCTTCGATCGGTAGCT.GGTC
 Dehlo._eth._(pin).seq CGTCCGATTAGCTAGTTGGTGGGGTAATGGCTACCAAGGCTTCGATCGGTAGCT.GGTC
 Dehlo._eth._(dll).seq CGTCCGATTAGCTAGTTGGTGGGGTAACGGCTACCAAGGCTTCGATCGGTAGCT.GGTC

FIG. 2-3

9/17

296 355
 E.coli.rnaB TGAGAGGATGACAGCCACACTGGAAGTGAACAGGTCAGACTCCTACGGAGGCAGC
 Deh_eth._.(cornell) TGAGAGGATGATCAGCCACACTGGGACTGAGACACGGGCCAGACTCCTACGGAGGCAGC
 Deh_eth._.(stf) TGAGAGGATGATCAGCCACACTGGGACTGAGACACGGGCCAGACTCCTACGGAGGCAGC
 Dehal_eth._.(pl).seq TGAGAGGATGATCAGCCACACTGGGACTGAGACACGGGCCAGACTCCTACGGAGGCAGC
 Dehlo_eth._.(dab).seq TGAGAGGATGATCAGCCACACTGGGACTGAGACACGGGCCAGACTCCTACGGAGGCAGC
 Dehlo_eth._.(pin).seq TGAGAGGATGATCAGCCACACTGGGACTGAGACACGGGCCAGACTCCTACGGAGGCAGC
 Dehlo_eth._.(dll).seq TGAGAGGATGATCAGCCACACTGGGACTGAGACACGGGCCAGACTCCTACGGAGGCAGC

356 415
 E.coli.rnaB AGTGGGGAATATTGCACAATGGCGCAAGCCTGATGCAGCCATGCCGCGTGTATGAAGAA
 Deh_eth._.(cornell) AGCAAGGAATCTTGGCAATGGCGAAAGCCTGACCCAGCAACGCCGCGTGAGGGATGAA
 Deh_eth._.(stf) AGCAAGGAATCTTGGCAATGGCGAAAGCCTGACCCAGCAACGCCGCGTGAGGGATGAA
 Dehal_eth._.(pl).seq AGCAAGGAATCTTGGCAATGGCGAAAGCCTGACCCAGCAACGCCGCGTGAGGGATGAA
 Dehlo_eth._.(dab).seq AGCAAGGAATCTTGGCAATGGCGAAAGCCTGACCCAGCAACGCCGCGTGAGGGATGAA
 Dehlo_eth._.(pin).seq AGCAAGGAATCTTGGCAATGGCGAAAGCCTGACCCAGCAACGCCGCGTGAGGGATGAA
 Dehlo_eth._.(dll).seq AGCAAGGAATCTTGGCAATGGCGAAAGCCTGACCCAGCAACGCCGCGTGAGGGATGAA

416 475
 E.coli.rnaB GGCTTCGGGTTGTAAAGTACTTTCAGCGGGAGGAAGGAGTAAGTTAATACCTTTGC
 Deh_eth._.(cornell) GGCTTCGGGTTGTAAACCTCTTTTCACAGGAAGAA.....TAAT.....
 Deh_eth._.(stf) GGCTTCGGGTTGTAAACCTCTTTTCACAGGAAGAA.....TAAT.....
 Dehal_eth._.(pl).seq GGCTTCGGGTTGTAAACCTCTTTTCACAGGAAGAA.....TAAT.....
 Dehlo_eth._.(dab).seq GGCTTCGGGTTGTAAACCTCTTTTCATAGGAAGAA.....TAAT.....
 Dehlo_eth._.(pin).seq GGCTTCGGGTTGTAAACCTCTTTTCATAGGAAGAA.....TAAT.....
 Dehlo_eth._.(dll).seq GGCTTCGGGTTGTAAACCTCTTTTCACAGGAAGAA.....TAAT.....

10/17

FIG. 2-4

476 E.coli.rnaB 535
 Deh_eth._(cornell) TCATTGACGTTACCCGACAGAAAGCACCGGCTAACTCCGTGCCAGCAGCCGCGGTAATA
 Deh_eth._(stf)GACGGTACCTGTGGAATAAGCTTCGGCTAACTACGTGCCAGCAGCCGCGGTAATA
 Dehal._eth._(pl)._seqGACGGTACCTGTGGAATAAGCTTCGGCTAACTACGTGCCAGCAGCCGCGGTAATA
 Dehlo._eth._(dab).seqGACGGTACCTGTGGAATAAGCTTCGGCTAACTACGTGCCAGCAGCCGCGGTAATA
 Dehlo._eth._(pin).seqGACGGTACCTGTGGAATAAGCTTCGGCTAACTACGTGCCAGCAGCCGCGGTAATA
 Dehlo._eth._(dll).seqGACGGTACCTGTGGAATAAGCTTCGGCTAACTACGTGCCAGCAGCCGCGGTAATA

536 E.coli.rnaB 594
 Deh_eth._(cornell) CGGAGGGT.GCAAGCGTTAATCGGAATTACTGGCGGTAAAGCGCAGCGGTTGTTC
 Deh_eth._(stf) CGTAGG.AAGCAAGCGTTATCCGGATTATTTGGCGGTAAAGTGAGCGTAGGTGCTTTTC
 Dehal._eth._(pl)._seq CGTAGG.AAGCAAGCGTTATCCGGATTATTTGGCGGTAAAGTGAGCGTAGGTGCTTTTC
 Dehlo._eth._(dab).seq CGTAGG.AAGCAAGCGTTATCCGGATTATTTGGCGGTAAAGTGAGCGTAGGTGCTTTTC
 Dehlo._eth._(pin).seq CGTAGG.AAGCAAGCGTTATCCGGATTATTTGGCGGTAAAGTGAGCGTAGGTGCTTTTC
 Dehlo._eth._(dll).seq CGTAGG.AAGCAAGCGTTATCCGGATTATTTGGCGGTAAAGTGAGCGTAGGTGCTTTTC

595 E.coli.rnaB 654
 Deh_eth._(cornell) AAGTCAGATGTGAAATCCCGGGCTCAACCTGGGAACGTGATCTGATACTGGCAAGCTTG
 Deh_eth._(stf) AAGTTGGATGTGAAATTTCCCGGCTTAACCGGACGTGTCAATCAATACTGTTGGACTAG
 Dehal._eth._(pl)._seq AAGTTGGATGTGAAATTTCCCGGCTTAACCGGACGTGTCAATCAATACTGTTGGACTAG
 Dehlo._eth._(dab).seq AAGTTGGATGTGAAATTTCCCGGCTTAACCGGACGTGTCAATCAATACTGTTGGACTAG
 Dehlo._eth._(pin).seq AAGTTGGATGTGAAATTTCCCGGCTTAACCGGACGTGTCAATCAATACTGTTGGACTAG
 Dehlo._eth._(dll).seq AAGTTGGATGTGAAATTTCCCGGCTTAACCGGACGTGTCAATCAATACTGTTGGACTAG

FIG. 2-5

11/17

655 714
E.coli.rnaB AGTCTCGTAGAGGGGTAGAATTCAGGTGTAGCGGTGAATGCCGTAGAGATCTGGAGG
Deh_eth._.(cornell) AGTACAGCAGGAGAAACCGAATTCCCGGTGTAGTGTAATAATGCCGTAGATATCGGGAGG
Deh_eth._.(stf) AGTACAGCAGGAGAAACCGAATTCCCGGTGTAGTGTAATAATGCCGTAGATATCGGGAGG
Dehal._eth._.(pl)._seq AGTACAGCAGGAGAAACCGAATTCCCGGTGTAGTGTAATAATGCCGTAGATATCGGGAGG
Dehlo._eth._.(dab)._seq AGTACAGCAGGAGAAACCGAATTCCCGGTGTAGTGTAATAATGCCGTAGATATCGGGAGG
Dehlo._eth._.(pin)._seq AGTACAGCAGGAGAAACCGAATTCCCGGTGTAGTGTAATAATGCCGTAGATATCGGGAGG
Dehlo._eth._.(dll)._seq AGTACAGCAGGAGAAACCGAATTCCCGGTGTAGTGTAATAATGCCGTAGATATCGGGAGG

715 774
E.coli.rnaB AATACCGGTGGCGAAGGCGGCCCTGGACGAAGACTGACGCTCAGGTGCCGAAAGCGTGG
Deh_eth._.(cornell) AACACCAGAGCGGAAGCGGTTTCTAGGTTGTCACTGACACTGAGGCTCGAAAGCGTGG
Deh_eth._.(stf) AACACCAGAGCGGAAGCGGTTTCTAGGTTGTCACTGACACTGAGGCTCGAAAGCGTGG
Dehal._eth._.(pl)._seq AACACCAGAGCGGAAGCGGTTTCTAGGTTGTCACTGACACTGAGGCTCGAAAGCGTGG
Dehlo._eth._.(dab)._seq AACACCAGAGCGGAAGCGGTTTCTAGGTTGTCACTGACACTGAGGCTCGAAAGCGTGG
Dehlo._eth._.(pin)._seq AACACCAGAGCGGAAGCGGTTTCTAGGTTGTCACTGACACTGAGGCTCGAAAGCGTGG
Dehlo._eth._.(dll)._seq AACACCAGAGCGGAAGCGGTTTCTAGGTTGTCACTGACACTGAGGCTCGAAAGCGTGG

755 834
E.coli.rnaB GGAGCAACACAGGATTAGATACCCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGT
Deh_eth._.(cornell) GGAGCGAACAGAAATTAGATACTCTGGTAGTCCACGCCCTTAAACTATGGACACTAGGTATA
Deh_eth._.(stf) GGAGCGAACAGAAATTAGATACTCTGGTAGTCCACGCCCTTAAACTATGGACACTAGGTATA
Dehal._eth._.(pl)._seq GGAGCGAACAGAAATTAGATACTCTGGTAGTCCACGCCCTTAAACTATGGACACTAGGTATA
Dehlo._eth._.(dab)._seq GGAGCGAACAGAAATTAGATACTCTGGTAGTCCACGCCCTTAAACTATGGACACTAGGTATA
Dehlo._eth._.(pin)._seq GGAGCGAACAGAAATTAGATACTCTGGTAGTCCACGCCCTTAAACTATGGACACTAGGTATA
Dehlo._eth._.(dll)._seq GGAGCGAACAGAAATTAGATACTCTGGTAGTCCACGCCCTTAAACTATGGACACTAGGTATA

12/17

FIG. 2-6

835
 E.coli.rnaB TGTGCCCTGAGCGTGGCTT.CCGAGCTAACGGTTAAGTCGACCGCCTGGGAGTAC 893
 Deh_eth._(cornell) GGGAGTATCGACCCCTCTGTGCGGAAAGCTAACGCTTTAAGTGTCCCGCCTGGGAGTAC
 Deh_eth._(stf) GGGAGTATCGACCCCTCTGTGCGGAAAGCTAACGCTTTAAGTGTCCCGCCTGGGAGTAC
 Dehal._eth._(pl)._seq GGGAGTATCGACCCCTCTGTGCGGAAAGCTAACGCTTTAAGTGTCCCGCCTGGGAGTAC
 Dehlo._eth._(dab).seq GGGAGTATCGACCCCTCTGTGCGGAAAGCTAACGCTTTAAGTGTCCCGCCTGGGAGTAC
 Dehlo._eth._(pin).seq GGGAGTATCGACCCCTCTGTGCGGAAAGCTAACGCTTTAAGTGTCCCGCCTGGGAGTAC
 Dehlo._eth._(dll).seq GGGAGTATCGACCCCTCTGTGCGGAAAGCTAACGCTTTAAGTGTCCCGCCTGGGAGTAC

901
 E.coli.rnaB GGCCGCAAGGTTAAACTCAAATGAATTGACGGGGGCGCCGACAAAGCGGTGGAGCAFGTG 953
 Deh_eth._(cornell) GGTCGCAAGGCTAAACTCAAAGGAATTGACGGGGGCGCCGACAAAGCAGCGGAGCGGTGTG
 Deh_eth._(stf) GGTCGCAAGGCTAAACTCAAAGGAATTGACGGGGGCGCCGACAAAGCAGCGGAGCGGTGTG
 Dehal._eth._(pl)._seq GGTCGCAAGGCTAAACTCAAAGGAATTGACGGGGGCGCCGACAAAGCAGCGGAGCGGTGTG
 Dehlo._eth._(dab).seq GGTCGCAAGGCTAAACTCAAAGGAATTGACGGGGGCGCCGACAAAGCAGCGGAGCGGTGTG
 Dehlo._eth._(pin).seq GGTCGCAAGGCTAAACTCAAAGGAATTGACGGGGGCGCCGACAAAGCAGCGGAGCGGTGTG
 Dehlo._eth._(dll).seq GGTCGCAAGGCTAAACTCAAAGGAATTGACGGGGGCGCCGACAAAGCAGCGGAGCGGTGTG

954
 E.coli.rnaB GTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATCCACGGA..AGTTTTC 1011
 Deh_eth._(cornell) GTTTAATTCGATGCTACACGAAGAAC.TTACCAAGATTTGACATGCATGAAGTAGTGAAC
 Deh_eth._(stf) GTTTAATTCGATGCTACACGAAGAACCTTACCAAGATTTGACATGCATGAAGTAGTGAAC
 Dehal._eth._(pl)._seq GTTTAATTCGATGCTACACGAAGAACCTTACCAAGATTTGACATGCATGAAGTAGTGAAC
 Dehlo._eth._(dab).seq GTTTAATTCGATGCTACACGAAGAACCTTACCAAGATTTGACATGCATGAAGTAGTGAAC
 Dehlo._eth._(pin).seq GTTTAATTCGATGCTACACGAAGAACCTTACCAAGATTTGACATGCATGAAGTAGTGAAC
 Dehlo._eth._(dll).seq GTTTAATTCGATGCTACACGAAGAACCTTACCAAGATTTGACATGCATGAAGTAGTGAAC

13/17

FIG. 2-7

1012
 E.coli.rnaB 1068
 AGAGATGAGAAATGTGCCCTTCGGG..AACCGTGAG.ACAGGTGCTGCATGGCTGTCGTCAG
 Deh_eth._.(cornell) CGAAGGGAAACGACCTGTTAAGTCAGGAGTTTGCACAGGTGCTGCATGGCTGTCGTCAG
 Deh_eth._.(stf) CGAAGGGAAACGACCTGTTAAGTCAGGAGTTTGCACAGGTGCTGCATGGCTGTCGTCAG
 Dehal._eth._(pl)._seq CGAAGGGAAACGACCTGTTAAGTCAGGAGTTTGCACAGGTGCTGCATGGCTGTCGTCAG
 Dehlo._eth._(dab).seq TGAAGGGGAACGACCTGTTAAGTCAGGAACTTGCACAGGTGCTGCATGGCTGTCGTCAG
 Dehlo._eth._(pin).seq TGAAGGGGAACGACCTGTTAAGTCAGGAACTTGCACAGGTGCTGCATGGCTGTCGTCAG
 Dehlo._eth._(dll).seq CGAAGGGGAACGACCTGTTAAGTCAGGAGTTTGCACAGGTGCTGCATGGCTGTCGTCAG

1069
 E.coli.rnaB 1128
 CTCGTGTTGTGAAATGTGGGTTAAGTCCCGCAACGAGCGCAACCCCTATCCTTTGTTGC
 Deh_eth._.(cornell) CTCGTGCCGTGAGGTGTTGGTTAAGTCCCGCAACGAGCGCAACCCCTATCCTTTGTTGC
 Deh_eth._.(stf) CTCGTGCCGTGAGGTGTTGGTTAAGTCCCGCAACGAGCGCAACCCCTATCCTTTGTTGC
 Dehal._eth._(pl)._seq CTCGTGCCGTGAGGTGTTGGTTAAGTCCCGCAACGAGCGCAACCCCTATCCTTTGTTGC
 Dehlo._eth._(dab).seq CTCGTGCCGTGAGGTGTTGGTTAAGTCCCGCAACGAGCGCAACCCCTATCCTTTGTTGC
 Dehlo._eth._(pin).seq CTCGTGCCGTGAGGTGTTGGTTAAGTCCCGCAACGAGCGCAACCCCTATCCTTTGTTGC
 Dehlo._eth._(dll).seq CTCGTGCCGTGAGGTGTTGGTTAAGTCCCGCAACGAGCGCAACCCCTATCCTTTGTTGC

1129
 E.coli.rnaB 1187
 CAGCGGTCCGGCCGGAACTCAAGGAGACTGCCAGTGATAAACTGG.AGGAAGGTGGGG
 Deh_eth._.(cornell) .AATTTTCTAGC.GAG.ACT..AGCGAGACTGCCCC.CGCGAAACGGGAGGAGGTGGGG
 Deh_eth._.(stf) .AATTTTCTAGC.GAG.....ACTGCCC.CGCGAAACGGGAGGAGGTGGGG
 Dehal._eth._(pl)._seq .AATTTTCTAGC.GAG.....ACTGCCC.CGCGAAACGGGAGGAGGTGGGG
 Dehlo._eth._(dab).seq .AATTTTCTAGC.GAG.....ACTGCCC.CGCGAAACGGGAGGAGGTGGGG
 Dehlo._eth._(pin).seq .AATTTTCTAGC.GAG.....ACTGCCC.CGCGAAACGGGAGGAGGTGGGG
 Dehlo._eth._(dll).seq .AATTTTCTAGC.GAG.....ACTGCCC.CGCGAAACGGGAGGAGGTGGGG

14/17

FIG. 2-8

1188
E.coli.rrnaB 1247
Deh_eth._.(cornell) ATGACGTCAAGTCATCATGGCCCTTACGACGAGGCTACACACGTGCTACAATGGCGCAT
Deh_eth._.(stf) ATGACGTCAAGTCAGCATGGCCCTTATATCTTGGGCTACACACACGCTACAATGGACAGA
Dehal._eth._.(pl)._seq ATGACGTCAAGTCAGCATGGCCCTTATATCTTGGGCTACACACGCTACAATGGACAGA
Dehlo._eth._.(dab)._seq ATGACGTCAAGTCAGCATGGCCCTTATATCTTGGGCTACACACGCTACAATGGACAGA
Dehlo._eth._.(pin)._seq ATGACGTCAAGTCAGCATGGCCCTTATATCTTGGGCTACACACGCTACAATGGACAGA
Dehlo._eth._.(dll)._seq ATGACGTCAAGTCAGCATGGCCCTTATATCTTGGGCTACACACGCTACAATGGACAGA

1248
E.coli.rrnaB 1307
Deh_eth._.(cornell) ACAATAGGTTGCAACAGTGTGAAGCTGAGCAAGCGGACCTCATAAAGTGCGTCCGTAGTCCGGAT
Deh_eth._.(stf) ACAATAGGTTGCAACAGTGTGAAGCTGAGCAAGCGGACCTCATAAAGTGCGTCCGTAGTCCGGAT
Dehal._eth._.(pl)._seq ACAATAGGTTGCAACAGTGTGAAGCTGAGCAAGCGGACCTCATAAAGTGCGTCCGTAGTCCGGAT
Dehlo._eth._.(dab)._seq ACAATAGGTTGCAACAGTGTGAAGCTGAGCAAGCGGACCTCATAAAGTGCGTCCGTAGTCCGGAT
Dehlo._eth._.(pin)._seq ACAATAGGTTGCAACAGTGTGAAGCTGAGCAAGCGGACCTCATAAAGTGCGTCCGTAGTCCGGAT
Dehlo._eth._.(dll)._seq ACAATAGGTTGCAACAGTGTGAAGCTGAGCAAGCGGACCTCATAAAGTGCGTCCGTAGTCCGGAT

1308
E.coli.rrnaB 1367
Deh_eth._.(cornell) TGGAGTCTGCAACTCGACTCCATGAAGTCGGAATCGTAGTAATCGTGGATCAGAATGCC
Deh_eth._.(stf) TGCAGGCTGAAACCCGCTGCATGAAGTTGGAGTTGCTAGTAACCGCATATCAGCAAGGT
Dehal._eth._.(pl)._seq TGCAGGCTGAAACCCGCTGCATGAAGTTGGAGTTGCTAGTAACCGCATATCAGCAAGGT
Dehlo._eth._.(dab)._seq
Dehlo._eth._.(pin)._seq
Dehlo._eth._.(dll)._seq

FIG. 2-9

WO 00/63443

15/17

PCT/US00/09883

1368
 E.coli.rrnaB ACGGTGAATACGTTCCGGGCTTGTACACACCGCCCGTCACACCATGGGAGTGGTTGC
 Deh_eth._.(cornell) GCGGTGAATACGTTCTCGGGCTTGTACACACCGCCCGTCACGTCATGANAGCCGGTAAC
 Deh_eth._.(stf) GCGGTGAATACGTTCTCGGGCTTGTACACACCGCCCGT
 Dehal_eth._.(pl)._seq
 Dehlo_eth._(dab).seq
 Dehlo_eth._(pin).seq
 Dehlo_eth._(dll).seq

1437
 E.coli.rrnaB AAAAGAAGTAGGTAGCTTAACCTTCGGGAGGGCGCTTACCACCTTGTGATTCATGACTGG
 Deh_eth._.(cornell) ACTTGAAGTCGATGTGCCAACCGCAAGGAGGACGTCGCCGAGGGTGGGACTGTAATTGG
 Deh_eth._.(stf)
 Dehal_eth._(pl)._seq
 Dehlo_eth._(dab).seq
 Dehlo_eth._(pin).seq
 Dehlo_eth._(dll).seq

1488
 E.coli.rrnaB GGTGAAGTCGTAACAAGGTAACCGTAGGGGAACCTGCCGTTGGATCACCCTCCTTA
 Deh_eth._.(cornell) GACGAAGTCGTAACAAGGTA
 Deh_eth._.(stf)
 Dehal_eth._(pl)._seq
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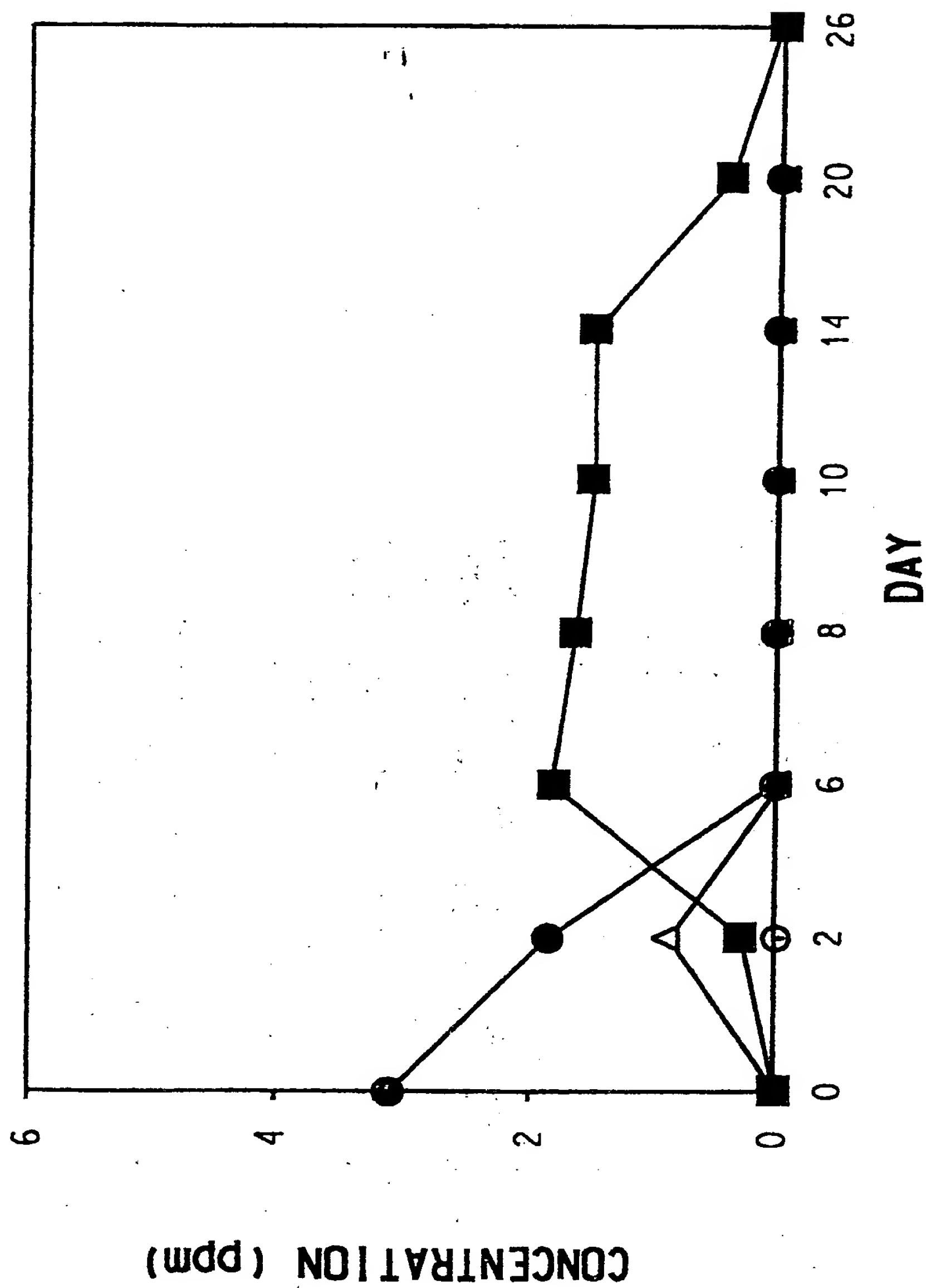
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 Seq. I.D. No.5
 Seq. I.D. No.6

16/17

PCE
TCE
DCE
VC

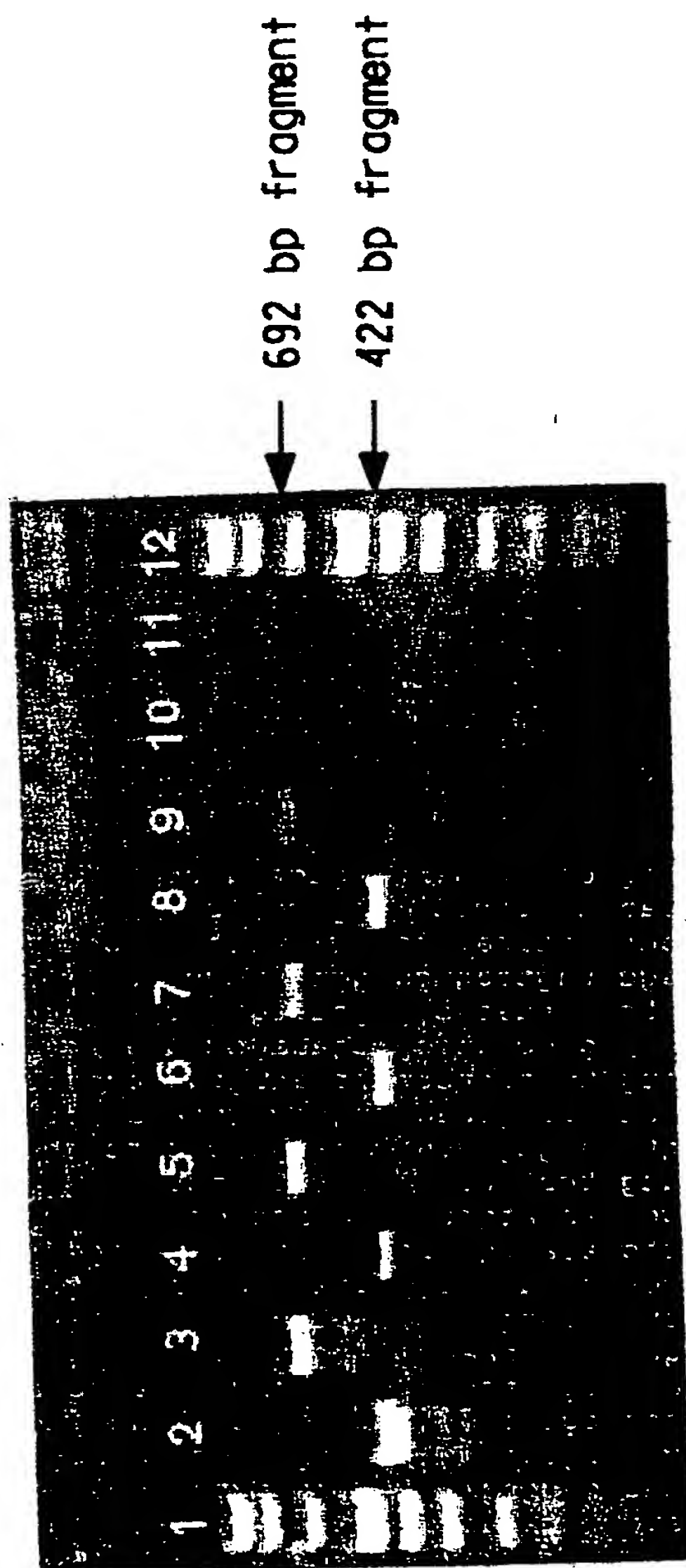
●
△
■
○

FIG. 3



17/17

FIG. 4



SEQUENCE LISTING

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DECHLORINATING BACTERIA

<130> BC1002 PCT

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<213> Dehalococcoides ethenogenes

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24

<210> 2

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<213> Dehalococcoides ethenogenes

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tgagagcta	at cc					1212

<210> 3

<211> 1335

<212> DNA

<213> Dehalococcoides ethenogenes

<400> 3

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caggagaaaa	cggaattccc	ggtgtagtgg	taaaatgcgt	agatatcggg	aggaacacca	660
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 <213> Dehalococcoides ethenogenes

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cggtacctgt	ggaataagct	tcggctaact	acgtgccagc	agccgcggtg	atacgtagga	480
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cagaattaga	tactctggta	gtccacgcct	taaactatgg	acactaggta	tagggagtat	780
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 <213> Dehalococcoides ethenogenes

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tggagcta	cc					1212

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 <212> DNA
 <213> Dehalococcoides ethenogenes

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gta 1443

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47

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20

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<210> 11
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<210> 13
<211> 20
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<220>
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aaatttaact agcaacaagg 20

<210> 14
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<210> 21
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<210> 24
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<220>
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<210> 29
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<220>
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